

Run on:	December 3, 2002, 14:35:53 ; Search time 35 Seconds (without alignments)
Title:	US-09-907-263-2
Perfect score:	941
Sequence:	1 DSVCPOGKYIHQNNSICCT.....CSNCKSLECTKLCUQIEN 161 612.953 Million cell updates/sec
Scoring table:	BLOSUM62
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Searched:	908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters:	908470
Post-processing:	Minimum Match 0% Maximum Match 100%
	Listing First 45 summaries
Database :	A_Geneseq_101002:*
	1: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1980.DAT:*
	2: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1981.DAT:*
	3: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1982.DAT:*
	4: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1983.DAT:*
	5: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1984.DAT:*
	6: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1985.DAT:*
	7: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1986.DAT:*
	8: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1987.DAT:*
	9: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1988.DAT:*
	10: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1989.DAT:*
	11: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1990.DAT:*
	12: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1991.DAT:*
	13: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1992.DAT:*
	14: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1993.DAT:*
	15: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1994.DAT:*
	16: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1995.DAT:*
	17: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1996.DAT:*
	18: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1997.DAT:*
	19: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1998.DAT:*
	20: /SIDS2/gcdata/geneseq/geneseq/emb1/AA1999.DAT:*
	21: /SIDS2/gcdata/geneseq/geneseq/emb1/AA2000.DAT:*
	22: /SIDS2/gcdata/geneseq/geneseq/emb1/AA2001.DAT:*
	23: /SIDS2/gcdata/geneseq/geneseq/emb1/AA2002.DAT:*
	RESULTS
	1 AAR27496
	2 ID AAR27496 standard; protein; 161 AA.
	3 XX
	4 AC AAR27496;
	5 DT 09-MAR-1993 (First entry)
	6 XX DE Native 30 kD TNF inhibitor.
	7 XX KW Tumour necrosis factor; ethylene glycol; pharmokinetic; adult respiratory distress syndrome; rheumatoid arthritis; septic shock; pulmonary fibrosis; spacer.
	8 XX Homo sapiens.
	9 XX WO9216221-A.
	10 XX PD 01-OCT-1992.
	11 XX PF 13-MAR-1992; 92WO-US02122.
	12 XX PR 15-MAR-1991; 91US-066962.
	13 XX PR 17-JUN-1992; 92US-0822296.
	14 XX PA (SYNDE) SYNERGEN INC.
	15 XX PI Armes LG, Breyer MT, Evans RJ, Kohno T, Thompson RC;
	16 XX DR WPI; 1992-348933/42.
	17 XX XX New ethylene glycolated polypeptide(s) with improved pharmacokinetic properties - for treating e.g. TNF and IL-1
	18 PT PT

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	941	100.0	161	13	AAR27496	Native 30 kD TNF i
2	941	100.0	161	19	AAW5664	Human soluble tumo
3	941	100.0	161	19	AAW5267	Soluble tumour nec
4	941	100.0	161	22	AAW8233	Tumour necrosis in
5	941	100.0	161	22	AAB31676	Human 30 kDa TNF i
6	941	100.0	211	20	AAW89225	Tumour necrosis fa
7	941	100.0	280	22	AAB65979	Tnfr protein. Un
8	941	100.0	309	16	AAR70108	TNF-R-GBP fusion
9	941	100.0	311	20	AAW9229	Tumour necrosis fa
10	941	100.0	336	18	AAW33360	TBP(20-190)/hCG-be

PT mediated diseases e.g. adult respiratory distress syndrome,  
 PT rheumatoid arthritis, septic shock etc.  
 XX

PS Claim 54; Fig 2; 10pp; English.

XX The sequence shows a native 30 kD TNF inhibitor which may be modified to contain at least one non-native cysteine residue, pref. at positions 1, 14, 105, 111 and/or 165. The non-native cysteine is joined to a non-peptidic polymer, pref. monomethoxy PEG via thio-ether bonds. Two such TNF inhibitor mols. may be linked via this non-peptidic spacer. The modified polypeptides show improved pharmacokinetic properties, i.e. increased mol. wt. hence reduced clearance rate following s.c. or systemic administration, increased sol. or native TNF inhibitors, and reduced antigenicity. The polypeptides may be used for treatment of TNF mediated diseases such as adult respiratory distress syndrome, pulmonary fibrosis, rheumatoid arthritis, inflammatory bowel disease and septic shock. The same method may be applied to the interleukin-1 receptor antagonist IL-1ra. See also AAR27495.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 13; Length 161;  
 Best Local Similarity 100.0%; Prod. No. 2.4e-67; Mismatches 0; Indels 0; Gaps 0;

Matches 161; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPGKYTHPQNSNICCTKCHGTYLYNDCPGPQDTCRCESESFTASBNHLRCL 60  
 Db 1 DSVCPGKYTHPQNSNICCTKCHGTYLYNDCPGPQDTCRCESESFTASBNHLRCL 60

Qy 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120  
 Db 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120

Qy 121 KONTVCTCHAGFFLRENECVSCKSSELECTKICLPOIEN 161  
 Db 121 KONTVCTCHAGFFLRENECVSCKSSELECTKICLPOIEN 161

RESULT 2  
 AAW5664  
 ID AAW5664 standard; Protein; 161 AA.  
 AC AAW5664;  
 DT 28-SEP-1998 (first entry)

XX Human soluble tumour necrosis factor receptor type I.

DE Human; tumour necrosis factor; TNF; TNF receptor type I; KW inflammatory disease; leukaemia; TNF binding protein; KW anti-inflammatory drug; methotrexates.

OS Homo sapiens.  
 XX WO9824463-A2.

PN 11-JUN-1998.

PD 11-JUN-1998.

XX 08-DEC-1997; 97WO-US22733.

XX 09-JUL-1997; 97US-005203.

PR 06-DEC-1996; 96US-003287.

PR 23-JAN-1997; 97US-0036355.

PR 07-FEB-1997; 97US-0033315.

XX (AMGE-) AMGEN INC.

XX Bendele AM, Edwards CK, Sennello RM;

XX WPI: 1998-333039/29.

DR N-PSDB; AAV41548.

PT Treatment of acute or chronic inflammatory disease, e.g. leukaemia -  
 PT by administering tumour necrosis factor binding protein and at least  
 PT one additional anti-inflammatory drug, e.g. methotrexate.  
 XX

PS Disclosure; Fig 1; 104pp; English.

XX This is the amino acid sequence of the human tumour necrosis factor receptor type I, used in the method of the invention involving the treatment of acute or chronic inflammatory disease such as leukaemia by administering tumour necrosis factor binding protein and at least one additional anti-inflammatory drug, e.g. methotrexate.  
 XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 19; Length 161;  
 Best Local Similarity 100.0%; Prod. No. 2.4e-67; Mismatches 0; Indels 0; Gaps 0;

Matches 161; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPGKYTHPQNSNICCTKCHGTYLYNDCPGPQDTCRCESESFTASBNHLRCL 60  
 Db 1 DSVCPGKYTHPQNSNICCTKCHGTYLYNDCPGPQDTCRCESESFTASBNHLRCL 60

Qy 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120  
 Db 61 SCSKCRKEMQVEISCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLNGTVHLSQE 120

Qy 121 KONTVCTCHAGFFLRENECVSCKSSELECTKICLPOIEN 161  
 Db 121 KONTVCTCHAGFFLRENECVSCKSSELECTKICLPOIEN 161

RESULT 3  
 AAW52267  
 ID AAW52267 standard; Protein; 161 AA.  
 XX  
 AC AAW52267;  
 DT 29-JUN-1998 (First entry)  
 XX  
 DE Soluble tumour necrosis factor receptor.  
 XX  
 KW Soluble tumour necrosis factor receptor; STNF-R; TNF-mediated disease;  
 KW tumour necrosis factor binding protein; autoimmune disease; arthritis;  
 KW adult respiratory distress syndrome; cachexia/anorexia; cancer; therapy;  
 KW chronic fatigue syndrome; graft rejection; Alzheimer's disease; TNFR.  
 XX  
 OS Homo sapiens.  
 XX WO9801555-A2.  
 XX 15-JAN-1998.  
 XX  
 PF 09-JUL-1997; 97WO-US12244.  
 XX  
 PR 04-MAR-1997; 97US-0039792.  
 PR 09-JUL-1996; 96US-0021443.  
 PR 06-DEC-1995; 96US-0032534.  
 PR 23-JAN-1997; 97US-0037337.  
 PR 07-FEB-1997; 97US-0039314.  
 XX  
 (AMGE-) AMGEN INC.

XX Edwards CK, Fisher EF, Kieft GL;

XX WPI; 1998-101052/09.

DR N-PSDB; AAV41548.

PT Truncated and soluble forms of tumour necrosis factor receptor -  
 PT useful for treating diseases involving factor, e.g. arthritis and  
 PT adult respiratory distress syndrome  
 XX

PS Claim 1; Fig 1; 205pp; English.

XX

This sequence is the human soluble tumour necrosis factor receptor (TNFR). The protein was used to make the truncated and tumour necrosis factor binding proteins (TNBP) are used to treat any TNF-mediated disease, e.g. arthritis, adult respiratory distress syndrome, cachexia/anorexia, cancer, chronic fatigue syndrome, graft rejection, Alzheimer's disease and other autoimmune diseases. Cells transformed with a vector containing DNA encoding the protein may be used for production of recombinant TNFR, which may also be used for measuring the amount of TNFR in samples and to raise antibodies against TNFR. TNBP may also be used in preparation of therapeutic compositions for treating the above diseases. The TNFR proteins are well suited to large scale production (since they lack the deamidation site in region 111-126, so are more stable *in vivo*); contain fewer disulphide bonds and fewer epitopes, making them less antigenic than full-length proteins.

SQ	Sequence	161 AA;
Query Match	100.0%;	Score 941; DB 19; Length 161;
Best Local Similarity	100.0%;	Pred. No. 2.4e-67;
Matches	161;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	D SVC PGK YTH P Q N N S I C C T K C H G T Y L Y N D C P G Q O D T D C R C E S G S F T A S E N H L R H C L 60
Db	1	D SVC PGK YTH P Q N N S I C C T K C H G T Y L Y N D C P G Q O D T D C R C E S G S F T A S E N H L R H C L 60
Qy	61	S C S K C R K E N G Q V E I S S C T V D R T V G C R K N Q Y H W S E N L F Q C F N C S L C L N G T V H L S C Q E 120
Db	61	S C S K C R K E N G Q V E I S S C T V D R T V G C R K N Q Y H W S E N L F Q C F N C S L C L N G T V H L S C Q E 120
Qy	121	K Q N T V C T C H A G F F L R E N E C V S C N N K S L E C T K L C L P Q I E N 161
Db	121	K Q N T V C T C H A G F F L R E N E C V S C N N K S L E C T K L C L P Q I E N 161

RESULT 4  
AAW9233  
ID AAW9233 standard; Protein; 161 AA.

XX AC

AAW9233;

XX DT 04-MAR-1999 (First entry)

XX DE Tumour necrosis inhibitor 30 kDa protein.

XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.

OS Homo sapiens.

XX PN WO949305-A1.

XX PD 05-NOV-1998.

XX PF 29-APR-1998; 98WO-US08631.

XX PR 01-MAY-1997; 97US-0850188.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Wooden S;

XX DR WPI; 1999-034661/03.

DR N-PSDB; AAU81732.

XX PT New chimeric osteoprotegerin polypeptides - contain the osteoprotegerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR mediated disorders

XX Disclosure; Fig 2; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising

CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated A1 monomers; (2) an isolated nucleic acid encoding A1; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transfected or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising CC tumour necrosis factor (TNF)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The CC chimeras are also useful for detecting molecules which interact with CC fused heterologous sequences to identify potential new receptors and CC ligands. The present sequence represents the TNF inhibitor 30 kDa protein.

SQ	Sequence	161 AA;
Query Match	100.0%;	Score 941; DB 20; Length 161;
Best Local Similarity	100.0%;	Pred. No. 2.4e-67;
Matches	161;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	D SVC PGK YTH P Q N N S I C C T K C H G T Y L Y N D C P G Q O D T D C R C E S G S F T A S E N H L R H C L 60
Db	1	D SVC PGK YTH P Q N N S I C C T K C H G T Y L Y N D C P G Q O D T D C R C E S G S F T A S E N H L R H C L 60
Qy	61	S C S K C R K E N G Q V E I S S C T V D R T V G C R K N Q Y H W S E N L F Q C F N C S L C L N G T V H L S C Q E 120
Db	61	S C S K C R K E N G Q V E I S S C T V D R T V G C R K N Q Y H W S E N L F Q C F N C S L C L N G T V H L S C Q E 120
Qy	121	K Q N T V C T C H A G F F L R E N E C V S C N N K S L E C T K L C L P Q I E N 161
Db	121	K Q N T V C T C H A G F F L R E N E C V S C N N K S L E C T K L C L P Q I E N 161

RESULT 5  
AAB37676  
ID AAB37676 standard; protein; 161 AA.  
XX AC AAB37676;  
XX DT 02-MAR-2001 (First entry)  
XX DE Human 30 kDa TNF inhibitor.  
XX KW TNF inhibitor; antiinflammatory; Tumour Necrosis Factor; interleukin; IL-1; inflammatory disease; degenerative disease; human.  
XX OS Homo sapiens.  
XX PN US613866-A.  
XX PD 07-NOV-2000.  
XX PF 19-JAN-1995; 95US-0375242.  
XX PR 19-JUL-1990; 90US-0555574.  
PR 09-JUL-1993; 93US-0090366.  
PR 18-JUL-1989; 89US-0381080.  
PR 11-DEC-1989; 89US-0450329.  
PR 07-FEB-1990; 90US-0479661.  
PA (AMGE-) AMGEN INC.

XX PI Squires C, King MW, Hale KK, Brewer MT, Thompson RC;
XX PI Vandervlice RW, Vannice J, Kohno T;
XX DR WPI; 2001-006443/01.
DR N-PSDB; AAC83945.
XX PT Novel 30 kDa tumor necrosis factor inhibitor analog comprising a non-native cysteine residue cross-linked with polyethylene glycol, useful for treating inflammatory and degenerative diseases mediated by

PT TNF -  
 XX  
 PS Claim 1; Fig 19; 82pp; English.

CC The present invention relates to Tumour Necrosis Factor (TNF) inhibitors  
 CC (see AAB3765 and AAB37685), which have TNF inhibitory activity. The  
 novel TNF inhibitors of the present invention are useful as therapeutic  
 agents for inhibiting the activity of TNF and interleukin (IL-1), and  
 CC for treating inflammatory and degenerative diseases mediated by TNF. The  
 CC 30 kDa TNF inhibitor can inhibit TNF alpha.

XX Sequence 161 AA;

Query Match 100.0%; Score 941; DB 22; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 AC 0; Gaps 0;  
 QY 1 DSVCPQGKVIHPORNSICCTKCHGTYLYNDCPGQDTCRBCESGSFTASEBNHLRHCL 60  
 Db 1 DSVCPQGKVIHPORNSICCTKCHGTYLYNDCPGQDTCRBCESGSFTASEBNHLRHCL 60  
 QY 61 SCSKRKEKMQVEITSCTVDRDITVGCRRKNQHYWSENLFQCPNCISLCLNGTVHLSQE 120  
 Db 61 SCSKRKEKMQVEITSCTVDRDITVGCRRKNQHYWSENLFQCPNCISLCLNGTVHLSQE 120  
 QY 121 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161  
 Db 121 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161

RESULT 6

ID AAWB9225 standard; Protein; 211 AA.  
 XX  
 AC AAWB9225;

XX 04-MAR-1999 (first entry)  
 DE Tumour necrosis factor bp/osteoprotegerin construct TNFBp 4.0.

XX Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 KW Homo sapiens.  
 OS Synthetic.  
 XX WO9849305-A1.  
 XX PD 05-NOV-1998.  
 XX PF 29-APR-1998; 98WO-US08631.  
 PR 01-MAY-1997; 97US-0850188.  
 XX (AMGE-) AMGEN INC.  
 PI Boyle WJ, Wooden S;  
 DR XX WPI; 1999-034601/03.

XX New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.

CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 acid encoding A1; (3) an expression vector comprising the nucleic acid  
 sequence; and (4) a host cell transformed or transfected with the

CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFBp/OPG construct from  
 CC the example of the present invention for creating TNFBp/OPG fusion  
 CC proteins.

XX Sequence 211 AA;

Query Match 100.0%; Score 941; DB 20; Length 211;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
 AC 0; Gaps 0;  
 QY 1 DSVCPQGKVIHPORNSICCTKCHGTYLYNDCPGQDTCRBCESGSFTASEBNHLRHCL 60  
 Db 41 DSVCPQGKVIHPORNSICCTKCHGTYLYNDCPGQDTCRBCESGSFTASEBNHLRHCL 100  
 QY 61 SCSKRKEKMQVEITSCTVDRDITVGCRRKNQHYWSENLFQCPNCISLCLNGTVHLSQE 120  
 Db 101 SCSKRKEKMQVEITSCTVDRDITVGCRRKNQHYWSENLFQCPNCISLCLNGTVHLSQE 160  
 QY 121 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161  
 Db 161 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 201

RESULT 7

ID AAB65979 standard; Protein; 280 AA.  
 XX  
 AC AAB65979;

XX 19-APR-2001 (first entry)  
 DE Tnfr1 protein.

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;  
 KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
 KW systemic lupus erythematosus; graft-versus-host disease; septic shock;  
 KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;  
 KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
 KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
 KW ischaemia; Parkinson's disease.  
 XX OS Unidentified.

XX PN WO200103719-A2.

XX PD 18-JAN-2001.

XX PN 07-JUL-2000; 2000WO-US18667.

XX PR 09-JUL-1999; 99US-0350670.

XX PR 09-DEC-1999; 99US-0457647.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX DR WPI; 2001-103031/11.

PT Treating conditions leading to bone loss such as rheumatoid arthritis,  
 PT multiple sclerosis and asthma, comprises administering an  
 PT osteoprotegerin protein in conjunction with e.g. inhibitors of  
 PT interleukin and tumor necrosis factor alpha -  
 XX Disclosure; Fig 2; 316pp; English.

The present invention relates to a method for treating conditions leading to bone loss. The method comprises administering a purified and isolated osteoprotegerin (OPG) protein (AAFF7836-AAFF7838 and AAB66974-AAB66976) in conjunction with other substances such as tumour necrosis factor-alpha (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet activating factor (PAF) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GvHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anoxia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock. The present sequence was used in a sequence homology comparison.

Sequence 280 AA;

Query Match	100.0%	Score 941; DB 22; Length 280;
Best Local Similarity	100.0%	Pred. No. 4e-67;
Matches	161; Conservative 0; Mismatches 0; Gaps 0;	
Qy	1 DSVCPGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 60	
Db	41 DSVCPGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 100	
Qy	61 SCSKCRKEMGOVEISSCTYDRTVGGCRKNQYRHWSNLFOQFNCSLCLNGTVHLSQE 120	
Db	101 SCSKCRKEMGOVEISSCTYDRTVGGCRKNQYRHWSNLFOQFNCSLCLNGTVHLSQE 160	
Qy	121 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161	
Db	161 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 201	

## RESULT 8

AAR70108  
ID AAR70108 standard; Protein; 309 AA.

AC AAR70108;

XX 10-NOV-1995 (first entry)

DE TNF-R-GBPH fusion protein.  
XX Hybrid peptide; malaria parasite; Plasmodium falciparum; fusion protein;  
XX red blood cell; cyclo receptor; glycoprotein binding peptide 130;  
KW GBP 130; GBPH; glycoprotein binding peptide homologue; glycoprotein A;  
KW tumour necrosis factor receptor; TNF-R.

OS Homo sapiens.

XX Chimeric Plasmodium falciparum.

FH Key Location/Qualifiers

FT Misc-difference 230...269  
/label= repeat-region  
FT /note= "can be repeated n times, where n is a real number"

XX WO9506737-A.

XX PD 09-MAR-1995.

XX PF 01-SEP-1994; 94WO-GB01900.

XX PR 03-SEP-1993; 93GB-0018350.

XX PR 23-AUG-1994; 94GB-0017021.

XX PA (PREN/) PRENDERGAST K F.

XX PI Prendergast K F;

XX PN

XX PD 09-NOV-1998.

XX PR 29-APR-1998;

XX PA 01-MAY-1997;

XX PA 98WO-US08631.

XX PI (AMGE-) AMGEN INC.

CC	XX	DR	WPI; 1995-115452/15.
CC	XX	PT	New hybrid peptide(s) for binding cytokine(s) - comprising a malaria parasite peptide capable of binding a red blood cell and a receptor peptide.
CC	XX	PT	
CC	XX	PS	Example A; Page 54-55; 93pp; English.
CC	XX	PS	Hybrid peptides for binding cytokines, comprising a malaria parasite (Plasmodium falciparum) peptide (capable of binding a red blood cell (RBC)) and a receptor peptide are claimed. AAR70103-25 are examples of these hybrid peptides. AAR70101 is a fusion of tumour necrosis factor receptor (in accordance with H Loescher et al Cell, Vol. 61, 351-359) and glycoprotein binding protein (GBP) homologue (GBP). The use of cytokine receptors not normally found on RBCs means that the cytokine can bind harmlessly to the RBC without deleterious effect.
CC	CC	CC	The RBC protects the hybrid peptides from excretion from the kidney, and due to steric hindrance prevents the cytokines binding to a receptor in another cell. GBP 130 or GBP are the 175 kDa erythrocyte binding antigen, used, others include EBA 175 (175 kDa erythrocyte binding antigen).
CC	CC	CC	PMMSA (pre major merozoite surface antigen) and the Duffy binding receptor molecule (eg. exhibited by Plasmodium vivax). These peptides bind to preI, glycophorin A, B and C, sialo glycoproteins, found on the surface of RBCs. The hybrid peptides are thus used to lower the levels of free cytokines in the circulation to reduce pathological damage.
CC	XX	XX	Sequence 309 AA;
Qy	Query Match	100.0%	Score 941; DB 16; Length 309;
Db	Best Local Similarity	100.0%	Pred. No. 4.4e-67;
Db	Matches	0; Mismatches 0; Indels 0; Gaps 0;	
Qy	Qy	1 DSVCPOGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 60	
Db	Db	20 DSVCPOGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 79	
Qy	Qy	1 DSVCPOGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 61	
Db	Db	80 DSVCPOGKYIHPQNSICCTKCHGTYLYNDCPGPQDDTCRCESGSFTASENHLRHCL 120	
Qy	Qy	121 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 161	
Db	Db	140 KQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN 180	
XX	XX	XX	RESULT 9
XX	XX	XX	AAW89229
XX	XX	XX	ID AAW89229 standard; Protein; 311 AA..
XX	XX	XX	AC AAW89229;
XX	XX	XX	DT 04-MAR-1999 (first entry)
XX	XX	XX	DE Tumour necrosis factor bp/osteoprotegerin construct TNFBp/304.
XX	XX	XX	KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.
XX	XX	XX	KW Homo sapiens.
XX	XX	XX	OS Synthetic.
XX	XX	XX	PN WO9819305-A1.
XX	XX	XX	PD 05-NOV-1998.
XX	XX	XX	PR 29-APR-1998;
XX	XX	XX	XX 01-MAY-1997;
XX	XX	XX	XX 97US-0850188.

PI Boyle WJ, Wooden S;  
XX WPI; 1999-034661/03.

DR N-PSDB; AAT94022.

XX  
PT New chimeric osteoprotegerin polypeptides - contain the  
osteoprotegerin dimerisation domain and a heterologous sequence,  
useful to treat TNF and TNFR-mediated disorders

PT XX  
PS Example 1; FIG 4; 92pp; English.

XX  
CC The present invention describes a chimeric polypeptide (Al), comprising  
an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
amino acid sequence. Also described are: (1) a multimer polypeptide  
comprising covalently associated Al monomers; (2) an isolated nucleic  
acid encoding Al; (3) an expression vector comprising the nucleic acid  
sequence, and (4) a host cell transformed or transfected with the  
expression vector so that the nucleic acid is expressible. The products  
from the present invention are useful to treat a variety of disorders  
including those related to receptor binding. Compositions comprising  
tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
are used to treat TNF and TNFR-mediated disorders such as inflammation,  
autoimmune diseases and disorders related to excessive apoptosis. The  
chimeras are also useful for detecting molecules which interact with  
fused heterologous sequences to identify potential new receptors and  
ligands. The present sequence represents a TNFbp/OPG construct from  
the example of the present invention for creating TNFbp/OPG fusion  
proteins.

XX Sequence 311 AA;

Query Match 100.0%; Score 941; DB 20; Length 311;

Best Local Similarity 100.0%; Pred. No. 4.4e-67; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0; Caps 0;

QY 1 DSVCPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRCBESGSFTASENHRLHCL 60

Db 41 DSVCPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRCBESGSFTASENHRLHCL 100

QY 61 SCSKCRKEMQVKEVSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSICLNSTVHLSQE 120

Db 101 SCSKCRKEMQVKEVSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSICLNSTVHLSQE 160

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLPOIEN 161

Db 161 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLPOIEN 201

RESULT 10  
AAW33360

ID AAW33360 standard; Protein; 336 AA.  
XX AC AAW33360;  
XX DT 19-MAR-1998 (first entry)

XX DE TBP(20-190)/hcg-beta fusion protein.  
XX KW Fusion protein; thrombopoietin; TPO; human chorionic gonadotrophin;  
KW beta subunit; hcg-beta.  
XX OS Homo sapiens.  
XX PN WO9730161-A1.  
XX PD 21-AUG-1997.

XX PR 20-FEB-1997; 97WO-US02315.

XX PR 20-FEB-1996; 96US-0011936.

XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX PI Campbell RK, Chappel SC, Jameson BA;

XX DR WPI; 1997-425036/39.  
XX PT Hybrid dimeric protein comprising two co-expressed units - each  
based on receptor or ligand and a subunit of a heterodimeric  
hormone, especially FSH, for inducing follicular maturation

XX PS Example; Pages 39-40; 60p; English.

XX  
CC A novel fusion protein comprises 2 dimer forming co-expressed amino  
acid sequences, each consisting of a homodimeric or heterodimeric  
receptor chain or ligand, with ligand-receptor binding activity,  
bound directly or via a peptide linker to a subunit of a heterodimer  
heterodimeric protein hormone capable of forming a heterodimer with  
the hormone's other subunits. The fusion protein, e.g. the  
thrombopoietin (TPO)/human chorionic gonadotrophin-beta subunit  
(hCG-beta) fusion protein denoted by the present sequence,  
significantly increases the biological activity of the hormone  
component, reducing the requirement for hormone itself and the  
number of injections needed.

XX Sequence 336 AA;

Query Match 100.0%; Score 941; DB 18; Length 336;

Best Local Similarity 100.0%; Pred. No. 4.7e-67; Indels 0; Gaps 0;  
Matches 161; Conservative 0; Mismatches 0; Caps 0;

QY 1 DSVCPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRCBESGSFTASENHRLHCL 60

Db 23 DSVCPQGVKIHPOQNSICCTKCHKGTYLYNDCPGQDPTCRCBESGSFTASENHRLHCL 82

QY 61 SCSKCRKEMQVKEVSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSICLNSTVHLSQE 120

Db 83 SCSKCRKEMQVKEVSCTVDRDTVGCRKNQRYHYWSNLFOCFNCSICLNSTVHLSQE 142

QY 121 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLPOIEN 161

Db 143 KONTVCTCHAGFFLRENECVSCSNCKSLECTKLPOIEN 183

RESULT 11  
AAW89228

ID AAW89228 standard; Protein; 366 AA.  
XX AC AAW89228;  
XX DT 04-MAR-1999 (first entry)

XX DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/248.  
XX KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
KW inflammation; apoptosis.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO989305-A1.

XX PD 05-NOV-1998.

XX PR 29-APR-1998; 98WO-US08631.

XX PR 01-MAY-1997; 97US-0850188.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Wooden S;

XX DR WPI; 1999-034661/03.

XX PT New chimeric osteoprotegerin polypeptides - contain the

PT osteoprotegerin dimerisation domain and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders  
 XX Example 1; Fig 4; 92pp; English.

XX The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimeric polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transformed or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNFR-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 XX Sequence 366 AA;

Query Match 100.0%; Score 941; DB 20; Length 366;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-67; Indels 0; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Gaps 0;  
 Sq Qy 1 DSVCPQGKYIHPQNNSICCTPKCHKGTYLYNDCPGPQDTDCRECEGSFTASENHLRHCL 60  
 Db 41 DSVCPQGKYIHPQNNSICCTPKCHKGTYLYNDCPGPQDTDCRECEGSFTASENHLRHCL 100  
 Qy 61 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 160  
 Qy 61 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 160  
 Qy 121 KONTVCTCHAGFFLRENECVCSNCCKSLECTKLQPQEN 161  
 Db 161 KONTVCTCHAGFFLRENECVCSNCCKSLECTKLQPQEN 201

RESULT 13 AAR07449 standard; protein; 397 AA.

XX ID AAW89227 standard; protein; 397 AA.

XX AC AAW89227;

XX DT 04-MAR-1999 (First entry)

XX DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.  
 XX DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.  
 XX DE Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX OS Homo sapiens.  
 OS Synthetic.

XX PF 98WO-US086331.  
 XX PR 01-MAY-1997; 97US-0850188.

XX PN WO9849305-A1.  
 XX PD 05-NOV-1998.  
 XX PI Boyle WJ, Wooden S;

XX PR 29-APR-1998; 98WO-US086331.  
 XX DR 01-MAY-1997; 97US-0850188.

XX PA (AMGEN INC.).  
 XX PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimer and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.  
 XX DR Hauptmann R, Himmier A, Maurer-Fogy I, Stratowa C;  
 XX PS N-PsDB; AAQ06282.  
 XX CC The present invention describes a chimeric polypeptide (A1), comprising

XX DNA encoding TNF binding protein and TNF- receptor - used in  
 PT tumour treatment and to understand mechanism to TNF action  
 PT XX Disclosure: Fig 1(1-3); 51pp; German.  
 PS XX Clone pTNF-BP1 was used to construct pADTNF-BP, for transfection of  
 CC e.g. COS7 cells. The expressed proteins are useful  
 CC prophylactically and therapeutically to control disorders which  
 CC involve the damaging effects of TNF-alpha or -beta (e.g. infectious or  
 CC parasitic diseases, shock, cachexia, autoimmune diseases, adult  
 CC respiratory distress syndrome etc., or side effects of treatment with  
 CC TNF-alpha). They can also be used as diagnostic reagents for  
 CC assaying TNF and in study of TNF-receptor interactions  
 CC See also AAQ06282-Q00285.

XX Sequence 371 AA;  
 Query Match 100.0%; Score 941; DB 11; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-67;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPQGKYIHPQNNSICCTPKCHKGTYLYNDCPGPQDTDCRECEGSFTASENHLRHCL 60  
 Db 41 DSVCPQGKYIHPQNNSICCTPKCHKGTYLYNDCPGPQDTDCRECEGSFTASENHLRHCL 100

Qy 61 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQVEISCTVDRDTVGCRKNQYRHWSENIFQCNCSLCLNGTVHLSQE 160

Qy 121 KONTVCTCHAGFFLRENECVCSNCCKSLECTKLQPQEN 161  
 Db 161 KONTVCTCHAGFFLRENECVCSNCCKSLECTKLQPQEN 201

RESULT 13

AAR07449

ID AAW89227

XX AC AAW89227;

XX DT 04-MAR-1999 (First entry)

XX DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/217.  
 XX DE Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin;  
 KW OPG; chimeric; fusion; dimerisation domain; autoimmune disease;  
 KW inflammation; apoptosis.  
 XX OS Homo sapiens.  
 OS Synthetic.

XX PF 98WO-US086331.  
 XX PR 01-MAY-1997; 97US-0850188.

XX PN WO9849305-A1.  
 XX PD 05-NOV-1998.

XX PI Boyle WJ, Wooden S;

XX PR 29-APR-1998; 98WO-US086331.  
 XX DR 01-MAY-1997; 97US-0850188.

XX PA (AMGEN INC.).  
 XX PT New chimeric osteoprotegerin polypeptides - contain the  
 PT osteoprotegerin dimer and a heterologous sequence,  
 PT useful to treat TNF and TNFR-mediated disorders

XX Example 1; Fig 4; 92pp; English.  
 XX DR Hauptmann R, Himmier A, Maurer-Fogy I, Stratowa C;  
 XX PS N-PsDB; AAQ06282.  
 XX CC The present invention describes a chimeric polypeptide (A1), comprising

an osteoprotegerin (OPG) dimerisation domain fused to a heterologous amino acid sequence. Also described are: (1) a multimer polypeptide comprising covalently associated Al monomers; (2) an isolated nucleic acid encoding Al; (3) an expression vector comprising the nucleic acid sequence; and (4) a host cell transformed or transfected with the expression vector so that the nucleic acid is expressible. The products from the present invention are useful to treat a variety of disorders including those related to receptor binding. Compositions comprising tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras are used to treat TNF and TNFR-mediated disorders such as inflammation, autoimmune diseases and disorders related to excessive apoptosis. The chimeras are also useful for detecting molecules which interact with fused heterologous sequences to identify potential new receptors and ligands. The present sequence represents a TNFbp/OPG construct from the example of the present invention for creating TNFbp/OPG fusion proteins.

XX  
SQ Sequence 397 AA;

Query	Match	Score	DB	Length
QY	1 DSVCPOGKYTHPQNNISCCTKCHKGTYLYNDCGPGQDTCRCECSSFTASENHRLCL	100.0%	20	397
Db	41 DSVCPOGKYTHPQNNISCCTKCHKGTYLYNDCGPGQDTCRCECSSFTASENHRLCL	100.0%	20	397
Qy	61 SCSKCRKEMQVESSCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLANGIVHUSCQE	120		
Db	101 SCSKCRKEMQVESSCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLANGIVHUSCQE	160		
Qy	121 KONTVCTCHAGFFRENECVSCSNCKSLECTKUCLPQIEN 161			
Db	161 KONTVCTCHAGFFRENECVSCSNCKSLECTKUCLPQIEN 201			

RESULT 14

AAW89226  
ID AAW89226 standard; Protein; 417 AA.

XX  
AC AAW89226;  
XX  
DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/196.  
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN W09849305-A1.

XX  
PD 05-NOV-1998.  
XX  
PP 29-APR-1998; 98WO-US08631.

XX  
PR 01-MAY-1997; 97US-0850188.  
XX  
(AMGE-) AMGEN INC.  
XX  
PI Boyle WJ, Wooden S;  
XX  
DR WPI; 1999-034661/03.

XX  
PT New chimeric osteoprotegerin polypeptides - contain the osteoprotgerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

XX  
PS Example 1; Fig 4; 92pp; English.

XX  
SQ Sequence 417 AA;

Query	Match	Score	DB	Length
QY	1 DSVCPOGKYTHPQNNISCCTKCHKGTYLYNDCGPGQDTCRCECSSFTASENHRLCL	100.0%	20	417
Db	41 DSVCPOGKYTHPQNNISCCTKCHKGTYLYNDCGPGQDTCRCECSSFTASENHRLCL	100.0%	20	417
Qy	61 SCSKCRKEMQVESSCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLANGIVHUSCQE	120		
Db	101 SCSKCRKEMQVESSCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCLANGIVHUSCQE	160		
Qy	121 KONTVCTCHAGFFRENECVSCSNCKSLECTKUCLPQIEN 161			
Db	161 KONTVCTCHAGFFRENECVSCSNCKSLECTKUCLPQIEN 201			

RESULT 15

AAW89224  
ID AAW89224 standard; Protein; 420 AA.

XX  
AC AAW89224;  
XX  
DT 04-MAR-1999 (first entry)

DE Tumour necrosis factor bp/osteoprotegerin construct TNFbp/OPG.  
KW Tumour necrosis factor receptor 1; TNFR-1; inhibitor; osteoprotegerin; OPG; chimeric; fusion; dimerisation domain; autoimmune disease; inflammation; apoptosis.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN W09849305-A1.

XX  
PD 05-NOV-1998.  
XX  
PP 29-APR-1998; 98WO-US08631.

XX  
PR 01-MAY-1997; 97US-0850188.  
XX  
(AMGE-) AMGEN INC.  
XX  
PI Boyle WJ, Wooden S;  
XX  
DR WPI; 1999-034661/03.

XX  
PT New chimeric osteoprotegerin polypeptides - contain the osteoprotgerin dimerisation domain and a heterologous sequence, useful to treat TNF and TNFR-mediated disorders

XX  
PS Example 1; Fig 4; 92pp; English.

XX  
 CC The present invention describes a chimeric polypeptide (A1), comprising  
 CC an osteoprotegerin (OPG) dimerisation domain fused to a heterologous  
 CC amino acid sequence. Also described are: (1) a multimer polypeptide  
 CC comprising covalently associated A1 monomers; (2) an isolated nucleic  
 CC acid encoding A1; (3) an expression vector comprising the nucleic acid  
 CC sequence; and (4) a host cell transfected or transfected with the  
 CC expression vector so that the nucleic acid is expressible. The products  
 CC from the present invention are useful to treat a variety of disorders  
 CC including those related to receptor binding. Compositions comprising  
 CC tumour necrosis factor (TNF)/OPG and TNF receptor (TNFR)/OPG chimeras  
 CC are used to treat TNF and TNF-mediated disorders such as inflammation,  
 CC autoimmune diseases and disorders related to excessive apoptosis. The  
 CC chimeras are also useful for detecting molecules which interact with  
 CC fused heterologous sequences to identify potential new receptors and  
 CC ligands. The present sequence represents a TNFbp/OPG construct from  
 CC the example of the present invention for creating TNFbp/OPG fusion  
 CC proteins.  
 XX

Sequence 420 AA:

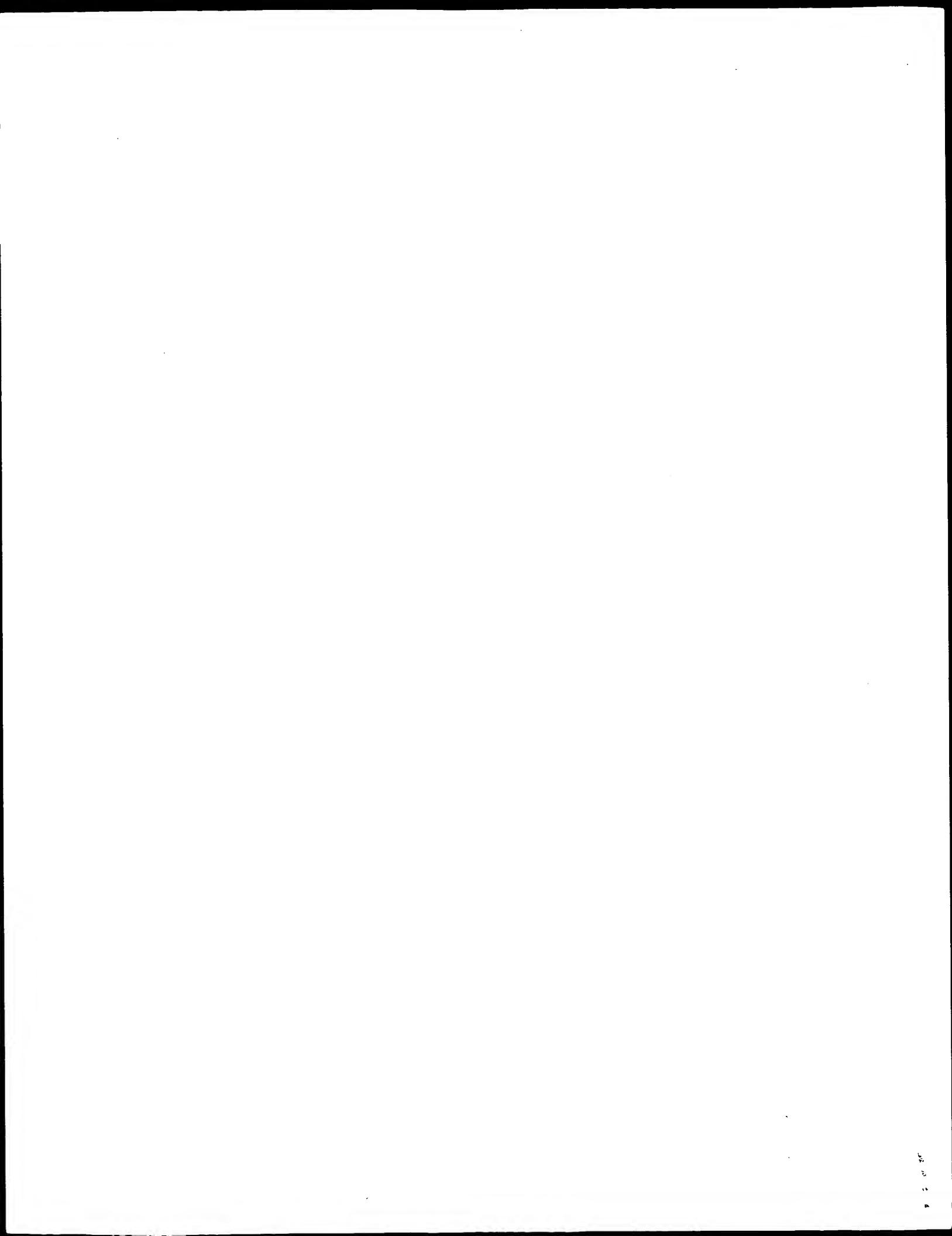
Score	941;	DB	20;	Length	420;
Query Match	100.0%;	Pred.	No.	5.8e-67;	
Best Local Similarity	100.0%;	Mismatches	0;	Indels	0;
Matches	161;	Conservative	0;	Gaps	0;

```

Qy      1 DSVCPQGKYIHPQQNSICCTKCHKGSTYLNDCPGPQDQTDCRECESGSPTASENHLRHCL 60
Db      41 DSVCPQGKYIHPQQNSICCTKCHKGTYLNDCPGPQDQTDCRECESGSPTASENHLRHCL 100
Qy      61 SCSKCRKEMGQEVEISSCTVDRDTVGCRKNQYRHYSENLFQOCNCNSLCLNGTVHLSQE 120
Db      101 SCSKCRKEMGQEVEISSCTVDRDTVGCRKNQYRHYSENLFQOCNCNSLCLNGTVHLSQE 160
Qy      121 KONTVCTCHAGFLENECVCSNCKSLECTKLQLPQEN 161
Db      161 KONTVCTCHAGFLENECVCSNCKSLECTKLQLPQEN 201

```

Search completed: December 3, 2002, 14:40:05  
 Job time : 37 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

4 protein - protein search, using sw model

an on: December 3, 2002, 14:39:28 ; Search time 15 Seconds  
(without alignment)  
315.8006 Million cell updates/sec

title:	score:	US-09-907-263-2
sequence:	1 DSVCPQSKYIHFQNNSICCT.....CSNCKKSLECTKLCIQLPQIEN 161	
oring table:	BLOGSUM62	
Gappp:	10.0 , Gapext 0.5	
arched:	262574 seqs, 29422922 residues	

total number of hits satisfying chosen parameters: 262574

minimum DB seq length: 0  
maximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB .pep:\*
- 2: /cgn2\_6/ptodata/1/iaa/5B --COMB .pep:\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB .pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB .pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTIS COMB .pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query	Match	Length	DB	ID	Description
1	941	100.0	161	4	US-09-326-394-2		Sequence 2, Appli
2	941	100.0	280	3	US-08-974-022-46		Sequence 46, Appli
3	941	100.0	280	4	US-08-795-445A-46		Sequence 46, Appli
4	941	100.0	280	4	US-08-795-447A-46		Sequence 46, Appli
5	941	100.0	280	4	US-08-974-186-46		Sequence 46, Appli
6	941	100.0	280	4	US-08-795-446B-46		Sequence 46, Appli
7	941	100.0	280	4	US-08-706-945D-132		Sequence 132, Appli
8	941	100.0	336	4	US-08-804-166-8		Sequence 8, Appli
9	941	100.0	336	4	US-08-910-991-8		Sequence 8, Appli
10	941	100.0	455	1	US-08-050-319B-25		Sequence 25, Appli
11	941	100.0	455	1	US-08-321-668-2		Sequence 2, Appli
12	941	100.0	455	1	US-08-837-041-2		Sequence 2, Appli
13	941	100.0	455	2	US-08-126-016-2		Sequence 2, Appli
14	941	100.0	455	2	US-08-465-982-25		Sequence 25, Appli
15	941	100.0	455	4	US-08-815-469-5		Sequence 5, Appli
16	941	100.0	455	4	US-08-006-353A-3		Sequence 3, Appli
17	941	100.0	455	4	US-08-527-236A-5		Sequence 4, Appli
18	941	100.0	455	4	US-08-054-970-2		Sequence 2, Appli
19	941	100.0	455	4	US-09-567-986-3		Sequence 4, Appli
20	941	100.0	455	4	US-09-013-895A-4		Sequence 3, Appli
21	930.5	98.9	909	4	US-09-442-868-4		Sequence 4, Appli
22	928	98.6	285	4	US-08-804-166-6		Sequence 6, Appli
23	928	98.6	285	4	US-09-910-991-6		Sequence 5, Appli
24	925.5	98.4	453	4	US-09-084-48A-5		Sequence 48, Appli
25	924	98.2	199	1	US-08-050-319B-48		Sequence 48, Appli
26	924	98.2	199	2	US-08-465-982-48		Sequence 48, Appli

ALIGNMENTS

RESULT 1  
US-09-326-394-2

```

; Sequence 2, Application US/09326394
; Patent No. 6306620
; GENERAL INFORMATION:
; APPLICANT: Bendele, Alison M.
; APPLICANT: Semenillo, Regina M.
; APPLICANT: Edwards, Carl K.
; TITLE OF INVENTION: COMBINATION THERAPY USING A TNF BINDING
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: CA
; COUNTRY: US
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; CURRENT APPLICATION NUMBER: US/09/326,394
; APPLICATION NUMBER: 08-DEC-1997
; FILING DATE: 08-DEC-1997
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,587
; FILING DATE: 06-DEC-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,355
; FILING DATE: 23-JAN-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/039,315
; FILING DATE: 07-FEB-1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 60/052,023
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,185
; REFERENCE DOCKET NUMBER: A-430D
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 161 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULAR TYPE: protein
; SEQ ID NO: 2
;
```

Query Match 100.0%; score 941; DB 4; Length 161;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative

RESULT 2  
 US-08-974-022-46  
 Sequence 46, Application US/08974022  
 Patent No. 6015938  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 COUNTRY: USA  
 ZIP: 91320-1789  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974, 022  
 FILING DATE: 12-DEC-1995  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/577, 788  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-974-022-46

Query Match 100.0%; score 941; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative

RESULT 3  
 US-08-795-445A-46  
 Sequence 46, Application US/08795445A  
 Patent No. 6284485  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: OSTEOPROTEGERIN  
 NUMBER OF SEQUENCES: 53  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Amgen Inc.  
 STREET: 1840 Dehavenland Drive  
 CITY: Thousand Oaks  
 STATE: California  
 ZIP: 91320-1789  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/795, 445A  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/577, 788  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Winter, Robert B.  
 REFERENCE/DOCKET NUMBER: A-378  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 280 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-795-445A-46

Query Match 100.0%; score 941; DB 3; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative

RESULT 4  
 US-08-795-447A-46  
 Sequence 46, Application US/08795447A  
 Patent No. 6284728  
 GENERAL INFORMATION:  
 APPLICANT: Boyle, William J.  
 APPLICANT: Lacey, David L.  
 APPLICANT: Calzone, Frank J.  
 APPLICANT: Chang, Ming-Shi  
 TITLE OF INVENTION: Osteoprotegerin

```

; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; STATE: Thousand Oaks
; COUNTRY: California
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-147A-46

Query Match          100  0%; Score 941; DB 4; Length 280;
Best Local Similarity 100  0%; Pred. No. 2.7e-76; Matches 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 DSVCPGKYIHPQNNSICCTKCHGTLYNDCPGPQDTDCRECEGSFTASENHLRHCL 60
Db   41 DSVCPGKYIHPQNNSICCTKCHGTLYNDCPGPQDTDCRECEGSFTASENHLRHCL 100
Qy   1 SCSKCRKEMQVEISSCTVDRDTVGCRKNQYHYSENLFQCFNCSLCLNGTVHLSQE 120
Db   101 SCSKCRKEMQVEISSCTVDRDTVGCRKNQYHYSENLFQCFNCSLCLNGTVHLSQE 160
Qy   121 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCPQEN 161
Db   161 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCPQEN 201
RESULT 6
US-08-795-446B-46
; Sequence 46, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Boyle, William J.
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-147A-46

Query Match          100  0%; Score 941; DB 4; Length 280;
Best Local Similarity 100  0%; Pred. No. 2.7e-76; Matches 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 DSVCPGKYIHPQNNSICCTKCHGTLYNDCPGPQDTDCRECEGSFTASENHLRHCL 60
Db   41 DSVCPGKYIHPQNNSICCTKCHGTLYNDCPGPQDTDCRECEGSFTASENHLRHCL 100
Qy   61 SCSKCRKEMQVEISSCTVDRDTVGCRKNQYHYSENLFQCFNCSLCLNGTVHLSQE 120
Db   101 SCSKCRKEMQVEISSCTVDRDTVGCRKNQYHYSENLFQCFNCSLCLNGTVHLSQE 160
Qy   121 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCPQEN 161
Db   161 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCPQEN 201
RESULT 5
US-08-974-186-46
; Sequence 46, Application US/08974186
; GENERAL INFORMATION:
; PATENT NO. 6284740
; ATTORNEY/AGENT INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,186
; FILING DATE:
; CLASSIFICATION:

```

Query Match Similarity 100.0%; Score 941; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYCPQSKYTHPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 60  
 Db 41 DSYCPQSKYVHPPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 100

QY 61 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 120  
 Db 101 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 160

QY 121 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 161  
 Db 161 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 201

RESULT 7

US-08-706-945D-132

; Sequence 132, Application US/08/0706945D

; Patent No. 6369027

; GENERAL INFORMATION:

; APPLICANT: Boyle, William

; APPLICANT: Lacey, David

; APPLICANT: Calzone, Frank

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: Osteoprotegerin

; FILE REFERENCE: A-378CIP

; CURRENT APPLICATION NUMBER: US/08/706, 945D

; CURRENT FILING DATE: 1996-09-03

; PRIORITY NUMBER: 08/155,777,788

; PRIOR FILING DATE: 1995-12-22

; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 132

; LENGTH: 280

; TYPE: PRT

; ORGANISM: Homo sapiens

US-08-706-945D-132

Query Match Similarity 100.0%; Score 941; DB 4; Length 280;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYCPQSKYTHPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 60  
 Db 41 DSYCPQSKYVHPPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 100

QY 61 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 120  
 Db 101 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 160

QY 121 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 161  
 Db 161 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 201

RESULT 8

US-08-804-166-8

; Sequence 8, Application US/08804166

; Patent No. 6193972

; GENERAL INFORMATION:

; APPLICANT: Campbell, Robert K.

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.

; NUMBER OF INVENTION: HYBRID PROTEINS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.

CITY: Washington  
 STATE: D.C.  
 ZIP: 22207

COMPILER READABLE FORM:

COMPUTER: IBM PC compatible  
 COMPUTER TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/804, 166

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/011, 936

FILING DATE: 20 February 1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Browdy, Roger L.

REGISTRATION NUMBER: 25, 618

REFERENCE DOCKET NUMBER: CAMPBELL=2A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-5197

TELEFAX: (202) 737-3528

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 336 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-804-166-8

Query Match Similarity 100.0%; Score 941; DB 4; Length 336;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-76; Mismatches 0; Indels 0; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSYCPQSKYTHPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 60  
 Db 23 DSYCPQSKYVHPPONNSICCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCL 82

QY 61 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 120  
 Db 83 SCSKRKEMGQEVSCTVDRDTVGCRKNQYRHYWSNLFQCFNCSLCLNGTVHLSQE 142

QY 121 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 161  
 Db 143 KQNTVCTCHAGFFIRENECVSCSNCKSLECLKLPOIEN 183

RESULT 9

US-08-910-991-8

; Sequence 8, Application US/08910991

; Patent No. 6194177

; GENERAL INFORMATION:

; APPLICANT: Campbell, Robert K.

; APPLICANT: Jameson, Bradford A.

; APPLICANT: Chappel, Scott C.

; TITLE OF INVENTION: HYBRID PROTEINS

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 CITY: Washington  
 STATE: D.C.

CITY: USA  
 ZIP: 22207

COMPILER READABLE FORM:

COMPUTER: IBM PC compatible  
 COMPUTER TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910, 991

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/804,166  
; FILING DATE: 20 February 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/011,936  
; FILING DATE: 20 February 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: YUN, Allen C.  
; REGISTRATION NUMBER: 37,971  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 336 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-050-319B-25

Query Match 100.0%; Score 941; DB 4; Length 336;  
Best Local Similarity 100.0%; Pred. No. 3.e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
US-08-050-319B-25  
Sequence 25, Application US/08050319B  
Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M. Brennan,  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
US-08-321-668-2  
Sequence 2, Application US/08321668  
GENERAL INFORMATION:  
APPLICANT: WALLACH, David  
APPLICANT: BRAKEBUSCH, Cord  
APPLICANT: VARFOLOMEY, Eugene  
APPLICANT: BATKIN, Michael  
TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/321,668  
FILING DATE: 12-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 107268  
FILING DATE: 12-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: WALLACH-13  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 244633  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-321-668-2

Query Match 100.0%; Score 941; DB 1; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 60  
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 100

QY 61 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 160

QY 121 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCLPQEN 161  
 Db 161 KONTVCTCHAGFIRENECVSCSNCKSLECLKLCLPQEN 201

RESULT 12  
 US-08-837-941-2 Application US/08837941  
 Sequence 2, Application US/08837941  
 Patent No. 5766917

GENERAL INFORMATION:  
 APPLICANT: WALLACH, David  
 APPLICANT: BRAKEBUSCH, Cord  
 APPLICANT: VARYOLOMEV, Eugene  
 APPLICANT: BATKIN, Michael  
 APPLICANT: AUBREK, DAN

TITLE OF INVENTION: MOLECULES INFLUENCING THE SHEDDING OF  
 TITLE OF INVENTION: THE TNF RECEPTORS, THEIR PREPARATION AND THEIR USE  
 NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Browdy and Neimark  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/837,941  
 FILING DATE: 28-APR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/321,668

FILING DATE: 12-OCT-1994  
 APPLICATION NUMBER: IL 107268  
 FILING DATE: 12-OCT-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: BROMY, Roger L.  
 NAME: BROMY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: WALLACH4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEX: 248633  
 FAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-837-941-2

TELEX: 241633  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 60  
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 100

QY 61 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 160

RESULT 13  
 US-08-126-016-2  
 Sequence 2, Application US/08126016  
 Patent No. 5811261

GENERAL INFORMATION:  
 APPLICANT: WALLACH, DAVID  
 APPLICANT: NOPHAR, YARON  
 APPLICANT: KEMPER, OLIVER  
 APPLICANT: ENGELMANN, HARTMUT  
 APPLICANT: BRAKEBUSCH, CORD

TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
 TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Browdy and Neimark  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/126,016  
 FILING DATE: 24-SEP-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/625668  
 FILING DATE: 13-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, ROGER L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: WALLACH4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEX: 248633  
 FAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 60  
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 100

QY 61 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 160

RESULT 14  
 US-08-126-016-2  
 Sequence 2, Application US/08126016  
 Patent No. 5811261

GENERAL INFORMATION:  
 APPLICANT: WALLACH, DAVID  
 APPLICANT: NOPHAR, YARON  
 APPLICANT: KEMPER, OLIVER  
 APPLICANT: ENGELMANN, HARTMUT  
 APPLICANT: BRAKEBUSCH, CORD

TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
 TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Browdy and Neimark  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/126,016  
 FILING DATE: 24-SEP-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/625668  
 FILING DATE: 13-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, ROGER L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: WALLACH4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEX: 248633  
 FAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 60  
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 100

QY 61 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 160

RESULT 15  
 US-08-126-016-2  
 Sequence 2, Application US/08126016  
 Patent No. 5811261

GENERAL INFORMATION:  
 APPLICANT: WALLACH, DAVID  
 APPLICANT: NOPHAR, YARON  
 APPLICANT: KEMPER, OLIVER  
 APPLICANT: ENGELMANN, HARTMUT  
 APPLICANT: BRAKEBUSCH, CORD

TITLE OF INVENTION: EXPRESSION OF THE RECOMBINANT TUMOR  
 TITLE OF INVENTION: NECROSIS FACTOR BINDING PROTEIN I (TBP-I)  
 NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Browdy and Neimark  
 STREET: 419 Seventh Street, N.W., Suite 300  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/126,016  
 FILING DATE: 24-SEP-1993  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/625668  
 FILING DATE: 13-DEC-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, ROGER L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: WALLACH4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEX: 248633  
 FAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 455 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-126-016-2

Query Match 100.0%; Score 941; DB 2; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-76; Gaps 0;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 60  
 Db 41 DSVCPQGKYTHPONNSICCTKCHKGTYLNDPGPGQDTCRCEGSFTASENHRLHCL 100

QY 61 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 120  
 Db 101 SCSKCRKEMGQEVSCTVDRDTVGCRKNQYRHWSBNLFQFCNSLCLNGTVHLSQE 160

RESULT 14  
US-08-465-982-25  
Sequence 25, Application US/08465982  
Patent No. 5863786  
GENERAL INFORMATION:  
APPLICANT: M. Feldmann, P.W. Gray,  
TITLE OF INVENTION: Modified human TNPalpha (Tumor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robbins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465, 982  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/050, 319  
FILING DATE: 10-May-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Robbins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-982-25

Query Match 100.0%; Score 941; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 60  
Db 41 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 100  
Db 61 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 120  
Qy 61 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 120  
Db 101 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 160  
Qy 121 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 201

Query Match 100.0%; Score 941; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 60  
Db 41 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 100  
Qy 61 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 120  
Db 101 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 160  
Qy 121 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 201

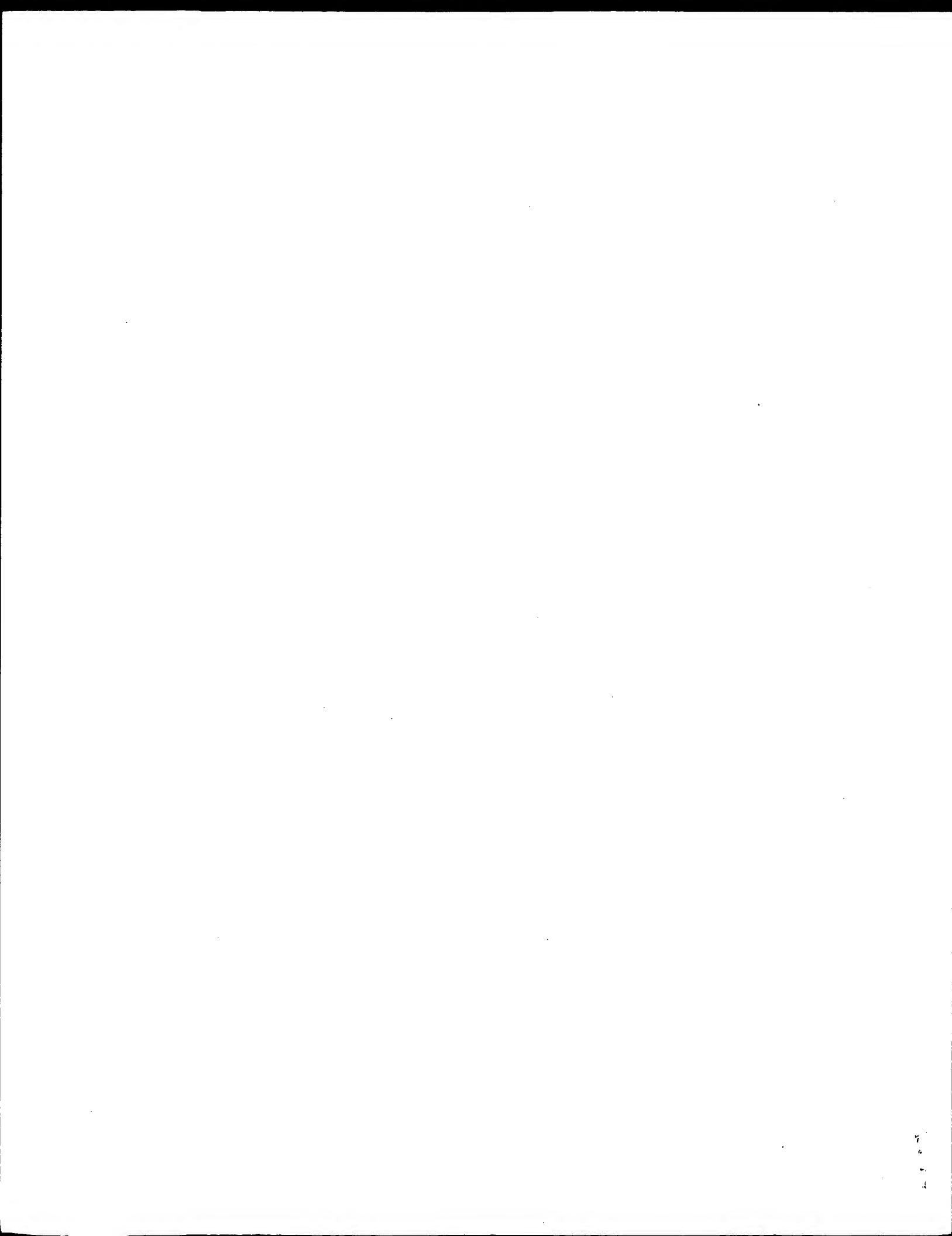
Search completed: December 3, 2002, 14:41:46  
Job time : 16 secs

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., NW, Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/815, 469  
FILING DATE: HEREWITH  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 6153402 Yet Assigned  
FILING DATE: 06-FEB-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028, 711  
FILING DATE: 17-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/013, 285  
FILING DATE: 12-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Steffe, Eric K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 455 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
US-08-815-469-5

Query Match 100.0%; Score 941; DB 4; Length 455;  
Best Local Similarity 100.0%; Pred. No. 4.3e-76;  
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 60  
Db 41 DSVCPOGKYTHPQQNSICCTKCHRGTYLYNDCPGQDTCRECESGSFTASENHLRHCL 100  
Qy 61 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 120  
Db 101 SCSKCRKEMGQVEISSCTVDRDTVGCCRKNQYRHWSENLFOCFCNSLCLNGTVHLSQE 160  
Qy 121 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 161  
Db 161 KONTVCTCHAGFFLRENECVSNCNCKSLECTKLCLPQIEN 201

RESULT 15  
US-08-815-469-5  
Patent No. 6153402  
GENERAL INFORMATION:  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Ni, Jian  
APPLICANT: Dixit, Vishva  
APPLICANT: Gentz, Reiner L.  
APPLICANT: Dillon, Patrick J.  
TITLE OF INVENTION: Death Domain Containing Receptors  
NUMBER OF SEQUENCES: 17



PAS soluble protein					
Copyright (c) 1993 - 2002 Compugen Ltd.					
protein - protein search, using sw model					
on: December 3, 2002, 14:39:03 ; Search time 17 Seconds (without alignments) 910.450 Million cell updates/sec					
title: US-0-9-907-263-2					
rfFact score: 941					
Sequence: 1 DSVCPQGYIHQNNSICCT.....CSNCKKSLECTKLCLPQIEN 161					
scoring table: BLOSUM62					
Gapop 10.0 , Gapext 0.5					
searched: 28324 seqs, 9614422 residues					
actual number of hits satisfying chosen parameters:	283224				
Minimum DB seq length: 0					
Maximum DB seq length: 2000000000					
DB processing: Minimum Match 0%					
Maximum Match 100%					
Listing first 45 summaries					
abase : PIR73:*					
1: Pir1:*					
2: Pir2:*					
3: Pir3:*					
4: Pir4:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.	283224				
SUMMARIES					
result 1					
QOHUTL tumor necrosis factor receptor 1 precursor [validated] - human					
N;Alternate names: P55 tumor necrosis factor receptor type 1					
N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor bindin					
C;Species: Homo sapiens (man)					
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 08-Dec-2000					
C;Accession: A38208; A34899; A36555; C36555; CD3000; F36555; G36555; T37316; T37316					
R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F.					
Genomics 13, 219-224, 1992					
A;Title: Structure of the human TNF receptor 1 (p60) gene (TNFR1) and localization					
A;Reference number: A38208; PMID:1315717					
A;Molecule type: DNA					
A;Residues: 1-455 <FUC>					
A;Cross-references: GB:M75861; GB:M75865; GB:M75866; NID:9339748; PMID:AAA6101					
R;Loetscher, H.; Pan, Y.C.E.; Lathm, H.W.; Gentz, R.; Brochhaus, M.; Tabuchi, H.					
Cell 61, 351-359, 1990					
A;Title: Molecular cloning and expression of the human tumor necrosis factor receptor 1 precursor					
A;Reference number: A38208; PMID:90235284; PMID:2158862					
A;Molecule type: mRNA					
A;Residues: 1-455 <LOE>					
A;Cross-references: GB:M58286; GB:M33480; NID:9339753; PMID:AAA6753.1; PID:93					
A;Experimental source: Placenta					
A;Note: part of this sequence, including the amino end of the mature protein.					
R;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Ga					
Cell 61, 361-370, 1990					
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor receptor 1 precursor					
A;Reference number: A34899; PMID:90235285; PMID:2158863					
A;Molecule type: mRNA					
A;Residues: 1-455 <SCH>					
A;Cross-references: GB:M32294; NID:9339744; PMID:AAA03210.1; PID:939745					
R;Himmeler, A.; Maurer-Poggy, I.; Kroenke, M.; Scheurich, P.; Pfizermaier, K.; L					
DNA Cell Biol. 9, 705-715, 1990					
A;Title: Molecular cloning and expression of human and rat tumor necrosis fact					
A;Reference number: A36555; PMID:91090841; PMID:1702293					
A;Molecule type: mRNA					
A;Residues: 1-455 <HIM>					
A;Cross-references: GB:M63121; NID:9339755; PMID:AAA36754.1; PID:9339756					
A;Molecule type: Protein					
A;Accession: C36555					
A;Note: the purified protein, called tumor necrosis factor binding protein, is					
R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.					
Proc. Natl. Acad. Sci. U.S.A. 87, 7880-7884, 1990					
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and express					
A;Reference number: A38281; PMID:91017509; PMID:2170974					
A;Molecule type: mRNA					

A;Residues: 1-455 <GRA>  
A;Cross-references: GB: M37764  
A;Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372  
R;Nophar, Y.; Kempf, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann  
EMBO J. 9, 3269-3278, 1990  
A;Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type  
 ie form of the receptor.  
A;Accession: S12057; MUID: 91006021; PMID: 1698610  
A;Molecule type: mRNA  
A;Residues: 1-455 <NOP>  
A;Cross-references: EMBL: X55313; NID: 93723; PIDN: CAA39021.1; PDB: 937224  
A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w  
R;Kemper, O.; Wallach, D.  
Gene 134, 209-216, 1993  
A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne  
A;Reference number: JTO758; MUID: 94085779; PMID: 8262379  
A;Accession: JTO758  
A;Molecule type: DNA  
A;Residues: 1-13 <KEM>  
R;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.  
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc  
A;Reference number: A60231; MUID: 90292116; PMID: 2113477  
A;Accession: A60231  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'X', 55-57 <SQC>  
R;Gatangwa, T.; Huang, C.; Kohr, W.; Capuccini, F.; Lucci III, J.A.; Jeffres, E.W.B.; Le  
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto  
 r) from patients.  
A;Reference number: A38258; MUID: 91062364; PMID: 2174164  
A;Molecule type: protein  
A;Residues: 41-60 <GAT>  
A;Experimental source: cancer patient serum  
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thyssell, H.; Grubb, A.; Adolf, G.  
Bur. J. Haematol. 42, 270-275, 1989  
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from  
A;Reference number: A60594; MUID: 89171156; PMID: 2924890  
A;Accession: A60594  
A;Molecule type: protein  
A;Residues: 41-43, 'X', 45-53, 'V', 55-57, 'XK' 60 <OLG>  
A;Experimental source: renal failure patient urine  
R;Engelmann, H.; Novick, D.; Wallach, D.  
J. Biol. Chem. 265, 1531-1536, 1990  
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence  
A;Reference number: A35010; MUID: 90110215; PMID: 2153136  
A;Accession: A35010  
A;Molecule type: protein  
A;Residues: 41-45 <ENG>  
A;Experimental source: normal urine  
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.  
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994  
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified f  
A;Reference number: JC2404; MUID: 95128033; PMID: 7765720  
A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53, 'X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
 C;Genetics: GDB: TNR1  
A;Cross-references: GDB: 125913; OMM: 191190  
A;Map position: 12p13.2-12p13.2  
A;Gene: TNR1  
A;Title: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-1/Domain: Signal sequence #status predicted <SIG>  
F;22-45/Domain: Signal sequence #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F;44-82/Domain: NGF receptor repeat homology <NG2>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-455/Domain: intracellular #status predicted <INT>

F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;27-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; MUID: 96011645; PMID: 7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: GB: U19994; NID: 9141752; PIDN: AAC48499.1; PID: 9141753  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SUT>  
A;Experimental source: kidney cell line 15  
A;Genetics:  
A;Gene: tnf  
C;Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor #status predicted <MAT>  
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: transmembrane #status predicted <MEM>  
F;211-231/Domain: transmembrane #status predicted <MEM>  
F;361-447/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 76.1%; Score 716.5; DB 2; Length 461;  
 Best Local Similarity 77.4%; Pred. No. 2e-45;  
 Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;  
 F;1-1/Domain: Signal sequence #status predicted <SIG>  
 F;22-45/Domain: Signal sequence #status predicted <MAT>  
 F;30-211/Domain: extracellular #status predicted <EXT>  
 F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F;44-82/Domain: NGF receptor repeat homology <NG1>  
 F;84-126/Domain: NGF receptor repeat homology <NG2>  
 F;168-196/Domain: NGF receptor repeat homology <NG3>  
 F;212-234/Domain: transmembrane #status predicted <MEM>  
 F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 100.0%; Score 941; DB 1; Length 455;  
 Best Local Similarity 100.0%; Pred. No. 8.3e-62;  
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 F;1-1/Domain: Signal sequence #status predicted <SIG>  
 F;22-45/Domain: Signal sequence #status predicted <MAT>  
 F;30-211/Domain: extracellular #status predicted <EXT>  
 F;41-201/Domain: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
 F;44-82/Domain: NGF receptor repeat homology <NG1>

RESULT 3

GOMST1 tumor necrosis factor receptor 1 precursor - mouse  
 C/N:Alternative names: tumor necrosis factor receptor, 55K  
 C/Species: Mus musculus (house mouse)  
 C/C Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 01-Dec-2000  
 C/C Accession: A38634; Tartaglia L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
 A/A/Title: Cloning and expression of cDNA's for two distinct murine tumor necrosis factor 1A/Reference number: A38634; MUID:91187885; PMID:1849278  
 A/A/Accession: A38634  
 A/Molecule type: mRNA  
 A/Residues: 1-454 <LEW>  
 A/Molecule type: mRNA  
 A/Residues: 1-454 <GO2>  
 A/Cross-references: GB:MG60468; NID:gi199825; PIDN:AAA39751.1; PID:gi199826  
 R/Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk  
 Mol. Cell. Biol. 11, 3020-3026, 1991  
 A/Tittle: Molecular cloning and expression of the type 1 and type 2 murine receptors for  
 A/Reference number: A40254; MUID:91246168; PMID:1645445  
 A/Accession: B40254  
 A/Molecule type: mRNA  
 A/Residues: 1-454 <BAR>  
 A/Cross-references: EMBL:X59238; NID:953578; PIDN:CBA41922.1; PID:gi53579  
 R/Barrett, K.; Taylor-Fishwick, D.A.; Brockhaus, M.; Gentz, R.; Lesslauer, W.  
 Eur. J. Immunol. 21, 1649-1656, 1991  
 A/Tittle: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis  
 A/Reference number: S16677; MUID:91285014; PMID:1647956  
 A/Accession: S16677  
 A/Molecule type: mRNA  
 A/Residues: 1-454 <ROT>  
 A/Cross-references: EMBL:X57796; NID:954848; PIDN:CAA40936.1; PID:gi54849  
 R/Bebo, B.F.  
 Immunogenetics 39, 450-451, 1994  
 A/Tittle: Nucleotide sequence of the TNF type I receptor from a mouse endothelium cell 1  
 A/Reference number: 154532; MUID:94245292; PMID:8185324  
 A/Accession: I54532  
 A/Molecule type: mRNA  
 A/Residues: 1-454 <RES>  
 A/Cross-references: GB:L26349; NID:gi430732; PIDN:AAA59361.1; PID:gi430733  
 R/Rothe, J.G.; Bluetmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.  
 Mol. Immunol. 30, 165-176, 1993  
 A/Tittle: Genomic organization and promoter function of the murine tumor necrosis factor  
 A/Reference number: I57826; MUID:93156721; PMID:8381516  
 A/Accession: I57826  
 A/Molecule type: DNA  
 A/Residues: 1-393, 'G', 395-454 <RE2>  
 A/Cross-references: GB:M76556; NID:gi202100; PIDN:AAA40465.1; PID:gi202102  
 C/Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca  
 C/Genetics:  
 A/Gene: TNFR-2  
 A/Introns: 13/3: 65/1: 108/1: 158/1; 184/2; 210/1; 249/1; 257/3; 353/1  
 C/Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology  
 C/Keywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein  
 F/F-1-29/Domain: signal sequence #status predicted <SIG>  
 F/F-30-454/Domain: tumor necrosis factor receptor type 1 #status predicted <SIG>  
 F/F-44-82/Domain: extracellular #status predicted <EXT>  
 F/F-44-82/Domain: NGF receptor repeat homology <NG1>  
 F/F-84-126/Domain: NGF receptor repeat homology <NG2>  
 F/F-127-167/Domain: NGF receptor repeat homology <NG3>  
 F/F-168-204/Domain: NGF receptor repeat homology <NG4>  
 F/F-213-235/Domain: transmembrane #status predicted <MEM>  
 F/F-236-454/Domain: intracellular #status predicted <INT>  
 F/F-54, 151-202/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	Score	DB	Length	454;
Best Local Similarity	71.3%	Pred.	No.	9.1e-43;
Matches	112;	Conservative	19;	Mismatches
Qy	1	DSVCPOGKYIHPQNNSICCTKCHKGTYLYNDCPGPQDIDTRECESGSPTASENHHLRHCL	60	;
Db	41	DNLCPQGKYIHPQNNSICCTKCHKGTYLYSDCOPSPGRDTVCRECEKGTFASQNYLVRQL	100	;
Qy	61	SCSKCRKENGQVEISSCTVDRDTIGCKRNQYRHWSNLFQCPNCNSLCLNGTYHLSQCB	120	;
Db	101	SCSKCRKEMSVQEISPCQADRTVCGCKENOFQRYLSETHFQCVDSPCFNGTVTPCKE	160	;
Qy	121	KONTVCTCHAGFFLRENECVCSNCNSKSLCTKLCLP	157	;
Db	161	TQNTVCNCHAGFFLRESECVPCSHCKKNECMKLCLP	197	;
RESULT 4				
GORTI1				
tumor necrosis factor receptor 1 precursor - rat				
N; Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)				
C; Species: Rattus norvegicus (Norway rat)				
C; Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 22-Jun-1999				
C; Accession: B36555				
R; Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lazarus, J.; DNA Cell Biol. 9:705-715, 1990				
A; Title: Molecular cloning and expression of human and rat tumor necrosis factor				
A; Reference number: A36555; PMID:91090811; PMID:1702293				
A; Accession: B36555				
A; Molecule type: mRNA				
A; Residues: 1-161 <HIM>				
A; Cross-references: GB:M63122; NID:9207361; PID:AAA42256_1; PID:9207362				
C; Comment: This protein is one of two known receptors for both TNF-alpha (cacheeotin) and TNF-beta (lymphotoxin). It is a type I transmembrane protein.				
C; Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homologous domain				
C; Keywords: duplication; glycoprotein; receptor; transmembrane protein				
F; 1-21/Domain: signal sequence #status predicted <SIG>				
F; 30-461/Domain: tumor necrosis factor receptor type 1 #status predicted <MAT>				
F; 30-211/Domain: extracellular #status predicted <EXT>				
F; 30-301/Domain: tumor necrosis factor binding protein #status predicted <PRO>				
F; 44-82/Domain: NGF receptor repeat homology <NG1>				
F; 84-126/Domain: NGF receptor repeat homology <NG2>				
F; 127-167/Domain: NGF receptor repeat homology <NG3>				
F; 168-204/Domain: NGF receptor repeat homology <NG4>				
F; 212-234/Domain: transmembrane #status predicted <MEM>				
F; 235-461/Domain: intracellular #status predicted <INT>				
F; 245-151/Domain: Binding site: carbohydrate (Asn) (covalent) #status predicted				
Query Match				
Best Local Similarity				
Matches				
110; Conservative				
18; Mismatches				
33; Indels				
0; Gaps				
0;				
Qy	1	DSVCPOGKYIHPQNNSICCTKCHKGTYLYNDCPGPQDIDTRECESGSPTASENHHLRHCL	60	;
Db	41	DNLCPQGKYIHPQNNSICCTKCHKGTYLYSDCOPSPGRDTVCRECEKGTFASQNYLVRQL	100	;
Qy	61	SCSKCRKENGQVEISSCTVDRDTIGCKRNQYRHWSNLFQCPNCNSLCLNGTYHLSQCB	120	;
Db	101	SCSKCRKEMSVQEISPCQADRTVCGCKENOFQRYLSETHFQCVDSPCFNGTVTPCKE	160	;
Qy	121	KONTVCTCHAGFFLRENECVCSNCNSKSLCTKLCLPQEIN	161	;
Db	161	KONTVCNCHAGFFLRESECVPCSHCKKNECMKLCLPPVAN	201	;
RESULT 5				
tumor necrosis factor receptor 2-related protein - human				
C; Species: Homo sapiens (man)				
C; Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000				
C; Accession: I54182				
R; Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Martynen, P.				
A; Title: Construction and evaluation of a cDNA library of human 120 transcribed				

A;Reference number: 154182; MUID:93252381; PMID:8286360  
A;Accession: IS4182  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-435 <RES>  
A;Cross-references: GB:L04270; NID:9339761; PIDN:AAA36757.1; PID:9339762  
C;Genetics:  
A;Gene: GJB:LTBR  
A;Map position: 12p13.3-12p13.1  
A;Cross-references: GDB:1230195; OMIM:600979  
C;Superfamily: tumor necrosis factor receptor repeat homology  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-42/Domain: nerve growth factor receptor #status experimental <MAT>  
F;29-50/Domain: extracellular #status predicted <EXT>  
A;Map position: 17q21-17q22  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-42/Domain: nerve growth factor receptor repeat homology <NG1>  
F;33-65/Domain: NGF receptor repeat homology <NG2>  
F;67-108/Domain: NGF receptor repeat homology <NG2>  
F;109-147/Domain: NGF receptor repeat homology <NG3>  
F;149-189/Domain: NGF receptor repeat homology <NG4>  
F;157-248/Region: serine/threonine-rich  
F;251-272/Domain: transmembrane #status predicted <TRM>  
F;273-427/Domain: intracellular #status predicted <INT>  
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 19.9%; Score 187.5; DB 2; Length 435;  
Best Local Similarity 32.7%; Pred. No. 7.4e-07; Matches 49; Conservative 17; MisMatches 71; Indels 13; Gaps 7;  
OY 8 KYIHPQNSNCTKCKGTYLYNDCPGPQDTCRECESFTASENHLHCLSKRK 67  
Db 164 NNHCVPCKAGHP - QNTSSPSARCQPHTR C 191  
RESULT 6 GOHUN  
nerve growth factor receptor precursor, low affinity [validated] - human  
N;Alternative name: NGF receptor  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text\_change 08-Dec-2000  
R.Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Moran, C.; Mercer, E.; Bothwell, M.  
Cell 47, 545-554, 1986  
A;Title: Expression and structure of the human NGF receptor.  
A;Reference number: A25218; MUID:87051725; PMID:3022937  
A;Accession: A25218  
A;Molecule type: mRNA  
A;Residues: 1-427 <JOH>  
A;Cross-references: GB:ML4764; NID:9189204; PIDN:AAA59541.1; PID:189205  
R.J.Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schatterman, G.; Thompson, S.; Grob, P.;  
J. Neurochem. 48, 225-232, 1987  
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth facto  
A;Reference number: A60204; MUID:87085574; PMID:3105363  
A;Accession: A60204  
A;Molecule type: protein  
A;Residues: 29-31, 'T', 33-42, 'TT', 45-46, 'TX', 50-51, 'XX', 54-56 <MAR>  
A;Experimental source: melanoma cell line A875  
A;Note: this sequence has been corrected by a note added in proof to follow the nucleot  
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goedke, J.; Ross, A.H.  
Arch. Biochem. Biophys. 294, 244-252, 1992  
A;Title: structural domains of the extracellular domain of human nerve growth factor rec  
A;Reference number: S21689; MUID:92198017; PMID:1372492  
A;Accession: S21689  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 183-206 <VIS>  
R;Sehgal, A.; Patel, N.; Chao, M.  
Mol. Cell. Biol. 8, 3160-3167, 1988  
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor  
A;Reference number: 157638; MUID:89096903; PMID:2850481  
A;Accession: 157638  
A;Molecule type: DNA  
A;Residues: 1-2 <RES>  
A;Cross-references: GB:M21621; NID:9189206; PIDN:AAA16363.1; PID:9189207  
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
C;Comment: This receptor undergoes both N- and O-linked glycosylation.  
C;Genetics:  
A;Gene: GDB:NGFR  
A;Cross-references: GDB:120234; OMIM:162010  
A;Map position: 17q21-17q22  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-42/Domain: nerve growth factor receptor repeat homology <NG1>  
F;33-65/Domain: NGF receptor repeat homology <NG2>  
F;67-108/Domain: NGF receptor repeat homology <NG2>  
F;109-147/Domain: NGF receptor repeat homology <NG3>  
F;149-189/Domain: NGF receptor repeat homology <NG4>  
F;157-248/Region: serine/threonine-rich  
F;251-272/Domain: transmembrane #status predicted <TRM>  
F;273-427/Domain: intracellular #status predicted <INT>  
F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 19.4%; Score 182.5; DB 1; Length 427;  
Best Local Similarity 32.1%; Pred. No. 1.7e-06; Matches 52; Conservative 25; MisMatches 62; Indels 23; Gaps 11;  
OY 4 CPQSKYIHPQNSNCTKCKGTYLYNDCPGPQDTCRECSFTASENHLHCLSKRK 62  
Db 32 CPTGlyTH--SGCKACAGLGEVAPC-GANQ-TWVCPCLSDVTSFVSVATERPCCR 86  
OY 63 SKCRKEMGQVEISS-CTVDRDTVGCRKNQRYHSENLFQCNCSLCLNGT-VHLICOB 120  
Db 87 TEC--VGLOMSAPCOVAADDAVRC--AVGYYDITGRCACRVCBAGSLVFSCQD 140  
Db 141 KQNTVCECPDGTVSDEANHVDPCLPCTVCDTERQLRBCTR 182  
RESULT 7 B38634  
tumor necrosis factor receptor type 2 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text\_change 23-Jul-1999  
C;Accession: B38634; A40545; S54816  
R;Lewis, M.; Tertaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,  
Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991  
A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor  
A;Reference number: A38634; MUID:91187885; PMID:1849278  
A;Accession: B38634  
A;Molecule type: mRNA  
A;Residues: 1-474 <LEW>  
A;Cross-references: GB:MC0469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Je  
Mol. Cell. Biol. 11, 3020-3026, 1991  
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors fo  
A;Reference number: A40254; MUID:91246168; PMID:1645445  
A;Accession: A40254  
A;Molecule type: mRNA  
A;Residues: 1-474 <GOO>  
A;Cross-references: GB:MG0469; NID:9199827; PIDN:AAA39752.1; PID:9199828  
R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y.  
submitted to the EMBL Data Library, May 1995  
A;Description: Characterization of the promoter region of the murine p75-TNF receptor.  
A;Reference number: S54816  
A;Accession: S54816  
A;Status: preliminary  
A;Molecule type: DNA  
A;Type: 1-22 <KIS>  
A;Cross-references: EMBL:187128; NID:9809043; PIDN:CAA60618.1; PID:9809044  
A;Residues: 1-22 <KIS>  
A;Cross-references: EMBL:187128; NID:9809043; PIDN:CAA60618.1; PID:9809044  
C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology  
C;Keywords: cytokine receptor; transmembrane protein  
F;1-22/Domain: signal sequence #status predicted <SIG>  
F;23-474/Domain: tumor necrosis factor receptor type 2 #status predicted <MAT>  
F;477-577/Domain: NGF receptor repeat homology <NG1>  
F;79-120/Domain: NGF receptor repeat homology <NG2>

P;166-203/Domain: NGF receptor repeat homology &lt;NG4&gt;

Query Match 19.2%; Score 181; DB 2; Length 474;  
Best Local Similarity 31.7%; Pred. No. 2, 3e-06;

Matches 51; Conservative 20; Mismatches 76; Indels 14; Gaps 8;

C:Species: myxoma virus

C:Accession: A40566

R/Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.

A;Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor.

A;Reference number: A40566; MUID:91335768; PMID:1651597

A;Molecule type: DNA

A;Residues: 1-326 &lt;UTP&gt;

A;Cross-references: GB:M95181; GB:M37976; PIDN:AA46632.1; PID:9332310

C:Keywords: glycoprotein

F;106-147/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;166-181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 179.5; DB 1; Length 326;  
Best Local Similarity 27.4%; Pred. No. 2, 3e-06;

Matches 51; Conservative 19; Mismatches 67; Indels 49; Gaps 7;

C:Species: myxoma virus T2 protein

C:Accession: A40566

R/Upton, C.; DeLange, A.M.; McFadden, G.

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 &lt;UTP&gt;

A;Cross-references: GB:M17413

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;61-105/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;106-147/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A26431; PHI1229 - revision 10-Sep-1999

R/Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.

Nature 325, 593-597, 1987

A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A;Reference number: A26431; MUID:87115839; PMID:307580

A;Accession: PHI1229

A;Molecule type: mRNA

A;Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

R/Metsis, M.; Tammusk, T.; Allikmets, R.; Sarma, M.; Sarma, M.;

A;Title: Regulatory elements and transcriptional regulation by the rat nerve growth factor receptor.

A;Reference number: PHI1229; MUID:93077038; PMID:146821

A;Accession: A26431

A;Molecule type: DNA

A;Residues: 1-425 &lt;RAD&gt;

A;Cross-references: GB:X051269

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells

Gene 121, 247-254, 1992

A;Title: The cysteine-rich region of the extracellular domain may form part or all of the receptor when it associates with it.

C:Genetics:

A;Introns: 20/3

A;Cross-references: GB:X121269

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;30-125/Domain: nerve growth factor receptor #status predicted &lt;MAT&gt;

F;30-251/Domain: extracellular #status predicted &lt;EXT&gt;

F;33-66/Domain: NGF receptor repeat homology &lt;NG1&gt;

F;68-109/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;110-148/Domain: NGF receptor repeat homology &lt;NG3&gt;

F;150-190/Domain: NGF receptor repeat homology &lt;NG4&gt;

F;198-249/Region: serine/threonine-rich

F;252-273/Domain: transmembrane #status predicted &lt;MEM&gt;

F;274-425/Domain: intracellular #status predicted &lt;INT&gt;

F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 176.5; DB 1; Length 425;

Best Local Similarity 30.9%; Pred. No. 4, 6e-06;

Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

C:Species: rabbit fibroma virus

C:Accession: B43692

R/Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 &lt;UTP&gt;

A;Cross-references: GB:M17413

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;61-105/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;106-147/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A26431; PHI1229 - revision 10-Sep-1999

R/Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.

Nature 325, 593-597, 1987

A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A;Reference number: A26431; MUID:87115839; PMID:307580

A;Accession: PHI1229

A;Molecule type: mRNA

A;Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

R/Metsis, M.; Tammusk, T.; Allikmets, R.; Sarma, M.; Sarma, M.;

A;Title: Regulatory elements and transcriptional regulation by the rat nerve growth factor receptor.

A;Reference number: PHI1229; MUID:93077038; PMID:146821

A;Accession: A26431

A;Molecule type: DNA

A;Residues: 1-425 &lt;RAD&gt;

A;Cross-references: GB:X051269

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells

Gene 121, 247-254, 1992

A;Title: The cysteine-rich region of the extracellular domain may form part or all of the receptor when it associates with it.

C:Genetics:

A;Introns: 20/3

A;Cross-references: GB:X121269

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;30-125/Domain: nerve growth factor receptor #status predicted &lt;MAT&gt;

F;30-251/Domain: extracellular #status predicted &lt;EXT&gt;

F;33-66/Domain: NGF receptor repeat homology &lt;NG1&gt;

F;68-109/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;110-148/Domain: NGF receptor repeat homology &lt;NG3&gt;

F;150-190/Domain: NGF receptor repeat homology &lt;NG4&gt;

F;198-249/Region: serine/threonine-rich

F;252-273/Domain: transmembrane #status predicted &lt;MEM&gt;

F;274-425/Domain: intracellular #status predicted &lt;INT&gt;

F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 176.5; DB 1; Length 425;

Best Local Similarity 30.9%; Pred. No. 4, 6e-06;

Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

C:Species: rabbit fibroma virus

C:Accession: B43692

R/Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 &lt;UTP&gt;

A;Cross-references: GB:M17413

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;61-105/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;106-147/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A26431; PHI1229 - revision 10-Sep-1999

R/Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.

Nature 325, 593-597, 1987

A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A;Reference number: A26431; MUID:87115839; PMID:307580

A;Accession: PHI1229

A;Molecule type: mRNA

A;Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

R/Metsis, M.; Tammusk, T.; Allikmets, R.; Sarma, M.; Sarma, M.;

A;Title: Regulatory elements and transcriptional regulation by the rat nerve growth factor receptor.

A;Reference number: PHI1229; MUID:93077038; PMID:146821

A;Accession: A26431

A;Molecule type: DNA

A;Residues: 1-425 &lt;RAD&gt;

A;Cross-references: GB:X051269

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells

Gene 121, 247-254, 1992

A;Title: The cysteine-rich region of the extracellular domain may form part or all of the receptor when it associates with it.

C:Genetics:

A;Introns: 20/3

A;Cross-references: GB:X121269

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;30-125/Domain: nerve growth factor receptor #status predicted &lt;MAT&gt;

F;30-251/Domain: extracellular #status predicted &lt;EXT&gt;

F;33-66/Domain: NGF receptor repeat homology &lt;NG1&gt;

F;68-109/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;110-148/Domain: NGF receptor repeat homology &lt;NG3&gt;

F;150-190/Domain: NGF receptor repeat homology &lt;NG4&gt;

F;198-249/Region: serine/threonine-rich

F;252-273/Domain: transmembrane #status predicted &lt;MEM&gt;

F;274-425/Domain: intracellular #status predicted &lt;INT&gt;

F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 176.5; DB 1; Length 425;

Best Local Similarity 30.9%; Pred. No. 4, 6e-06;

Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

C:Species: rabbit fibroma virus

C:Accession: B43692

R/Upton, C.; DeLange, A.M.; McFadden, G.

Virology 160, 20-30, 1987

A;Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric

A;Reference number: A43692; MUID:87321103; PMID:2820128

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-325 &lt;UTP&gt;

A;Cross-references: GB:M17413

C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F;61-105/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;106-147/Domain: NGF receptor repeat homology &lt;NG3&gt;

Query Match 18.9%; Score 178; DB 2; Length 325;

Best Local Similarity 29.6%; Pred. No. 3e-06;

Matches 45; Conservative 15; Mismatches 62; Indels 30; Gaps 6;

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A26431; PHI1229 - revision 10-Sep-1999

R/Radeke, M.J.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.

Nature 325, 593-597, 1987

A;Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.

A;Reference number: A26431; MUID:87115839; PMID:307580

A;Accession: PHI1229

A;Molecule type: mRNA

A;Cross-references: GB:X05137; NID:956755; PIDN:CAA28783.1; PID:956756

R/Metsis, M.; Tammusk, T.; Allikmets, R.; Sarma, M.; Sarma, M.;

A;Title: Regulatory elements and transcriptional regulation by the rat nerve growth factor receptor.

A;Reference number: PHI1229; MUID:93077038; PMID:146821

A;Accession: A26431

A;Molecule type: DNA

A;Residues: 1-425 &lt;RAD&gt;

A;Cross-references: GB:X051269

C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells

Gene 121, 247-254, 1992

A;Title: The cysteine-rich region of the extracellular domain may form part or all of the receptor when it associates with it.

C:Genetics:

A;Introns: 20/3

A;Cross-references: GB:X121269

C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; transmembrane

F;1-29/Domain: signal sequence #status predicted &lt;SIG&gt;

F;30-125/Domain: nerve growth factor receptor #status predicted &lt;MAT&gt;

F;30-251/Domain: extracellular #status predicted &lt;EXT&gt;

F;33-66/Domain: NGF receptor repeat homology &lt;NG1&gt;

F;68-109/Domain: NGF receptor repeat homology &lt;NG2&gt;

F;110-148/Domain: NGF receptor repeat homology &lt;NG3&gt;

F;150-190/Domain: NGF receptor repeat homology &lt;NG4&gt;

F;198-249/Region: serine/threonine-rich

F;252-273/Domain: transmembrane #status predicted &lt;MEM&gt;

F;274-425/Domain: intracellular #status predicted &lt;INT&gt;

F;61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.8%; Score 176.5; DB 1; Length 425;

Best Local Similarity 30.9%; Pred. No. 4, 6e-06;

Matches 50; Conservative 25; Mismatches 68; Indels 19; Gaps 10;

C:Species: rabbit fibroma virus

Qy 63 SKCRKEMGQVEITS-CIVDRTDTCVGGKRKNQVRHYSNLFQCFNSLCLNGT-VHLSCOE 120  
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 88 TBC--LGLQMSAPCWEADDAVRC--AVGYQDEETGHCEACSVCEVGSGUVFSCQD 141.

Qy 121 KONTVVC-TCHAGFFFLPE---NECYCSNCNCKSLECTKLCLP 157  
 |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
 Db 142 KONTVVCBECPEGTYSDDEANHVDPPLCPCTVCEDTEROLRECTP 183

RESULT 11

gene murine tumor necrosis factor receptor 2 protein - mouse (fragment)

C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 23-Jul-1999

C;Accession: I48854 R; Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.

Mamm. Genome 5, 726-727, 1994  
 A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.

A;Reference number: I48854; MUID:95178848; PMID:767384

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA  
 A;Residues: I-459 <RES>

A;Cross-references: EMBL:X16401; PIDN:GA5981.1; PID:943831  
 C;Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology <NGF>  
 F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

Query Match 18.7%; Score 176; DB 2; Length 459;

Best Local Similarity 31.1%; Pred. No. 5.3e-06; Matches 50; Conservative 20; Mismatches 77; Indels 14; Gaps 8;

C;Comment: For an alternative splice form, see PIR:A46476.  
 C;Superfamily: CP27 antigen; NGF receptor repeat homology  
 C;Keywords: alternative splicing; transmembrane protein  
 F;105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 17.8%; Score 167.5; DB 2; Length 305;  
 Best Local Similarity 29.9%; Pred. No. 1.7e-05; Matches 46; Conservative 23; Mismatches 72; Indels 13; Gaps 7;

Db 26 CSQKYLH--DQCCDLQPOSRLTSHTML-EKQCHCFDSGERFSAQNNRERCHOHR 81

Db 64 KCRKEMGQVEITSCTVVDRTDTCVGGKRKNQYRHYSENLFQCFNSLCLNG-TVHLSCOEKO 122

Db 82 HCEPNQGLRKKEGTAFESDTVCKEGO-Q-HCTSKEACEAQHTCPAIPGFGVUMEMATT 139

Db 123 NTIV-TCHAGFFELR---EVSCSNCK-SLEKTLCLP 150

Db 140 DTVCHPCPVGFSSNOSSLIFERKCYPWTSCEDKMLE 173

RESULT 13

D72175 G2R protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence\_revision 24-Nov-1999 #text\_change 20-Jun-2000

C;Accession: D72175 R;Sicheleikunov, S.N.; Totmenin, A.V.; Gutovov, V.V.; Safronov, P.F.; Massung, R.F.; Iopai submitted to GenBank, March 1998

A;Reference number: A72150 A;Experimental source: strain Garcia-1966

A;Status: preliminary

A;Molecule type: DNA

A;Residues: I-349 <SHC>

A;Cross-references: GB:Y16780; PIDN:9583055; PIDN:CA854798.1; PID:95830759

A;Experimental source: strain Garcia-1966

A;Gene: G2R

C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

Query Match 17.7%; Score 166.5; DB 2; Length 349;

Best Local Similarity 26.7%; Pred. No. 2.2e-05; Matches 46; Mismatches 64; Indels 43; Gaps 9;

T28623 hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 21-Jul-2000

C;Accession: T28623 R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.; Immunol. 149, 3921-3926, 1992

A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.

A;Reference number: A46515; MUID:93094586; PMID:1281194

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: I-287, 'LV' <GRI>

A;Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N

A;Experimental source: BALB/c, liver

A;Note: sequence extracted from NCBI backbone (NCBIP:120357)

C;Comment: For an alternative splice form, see PIR:A46515.

A;Cross-references: GB:M83312; NID:91553058

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: I-287, 'LV' <GRI>

A;Cross-references: GB:M83312; NID:91553058; PIDN:AAB08705.1; PID:91553059; GB:M94126; N

A;Experimental source: BALB/c, liver

A;Note: sequence extracted from NCBI backbone (NCBIP:120357)

C;Comment: For an alternative splice form, see PIR:A46515.

A: Cross-references: EMBL:U22579; PIDN:AAA60933\_1; PID:g439102  
 A: Experimental source: strain Bangladesh 1975  
 C: Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 4: Score 17.4%; DB 2; Length 348;  
 Best Local Similarity 27.8%; Pred. No. 3.3e-05;  
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

Qy 4 CPQGKYIHPQNNSICCTKCHGTYLYNDCPGQQDDCREEGSFTTASNNHLRHCLSCS 63

Db 31 CKDTEY--KRHNLCCLSCCPPTYASRLCDSK-TNTQCTCGSGFTTSNNHHLPAULSCN 86

Qy 64 -KCRKEMGQEVISSCTVDRDTVGCRKNOVRHYWSENLFQCF----NC5LCLNGTVHLS 117

Db 87 GR CNS -NQVETRSCTNTHNRCECSPGYY-----CLWKSSGGCKACVST--- 130

Qy 118 CQEKQNTVCTCHAGFFLRENECVS--CSNC 145

Db 131 -----KCIGYGVSIGHTSGVGDVTCSPC 152

## RESULT 15

D36858 Gene G4R protein - variola virus

N: Alternate names: B29R protein (COP)

C: Species: variola virus

C: Date: 30-Sep-1993 #Sequence revision 30-Sep-1993 #text\_change 23-Mar-2001  
 C: Accession: D36858; S46888; S32385; S35987

R: Blinov, V.M.

submitted to GenBank, November 1992

A: Reference number: A36859

A: Accession: D36858

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-349 <BLI>

A: Cross-references: GB:X69198; PIDN:9456758; PIDN:CAA49137\_1; PID:9457087

A: Experimental source: strain India-1967 ssp. major isolate Ind3  
 R: Shchelkunov, S.N.; Blinov, V.M.; Gytrov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Frolov, V.V.

Submitted to the EMBL Data Library, April 1992

A: Description: Nucleotide sequence analysis of the region of Variola virus XHOI F O H P

A: Accession: S46888

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-349 <KOL>

A: Cross-references: EMBL:X67117; PIDN:9516428; PIDN:CAA47540\_1; PID:9516449

A: Experimental source: strain India-1967, isolate Ind3

R: Shchelkunov, S.N.; Blinov, V.M.; Sandatkhiev, L.S.

FEBS Lett. 319, 80-83, 1993

A: Title: Genes of variola and vaccinia viruses necessary to overcome the host protective

A: Reference number: S32385; MUID:9340228; PMID:8384129

A: Accession: S32385

A: Molecule type: DNA

A: Residues: 31-168 <SHC>

A: Cross-references: EMBL:X69198

A: Experimental source: strain India-1967, ssp. major

C: Genetics:

A: Gene: G4R

C: Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

F: 32-66/Domain: NGF receptor repeat homology <NGF>

F: 168-109/Domain: NGF receptor repeat homology <NG2>

F: 110-151/Domain: NGF receptor repeat homology <NG3>

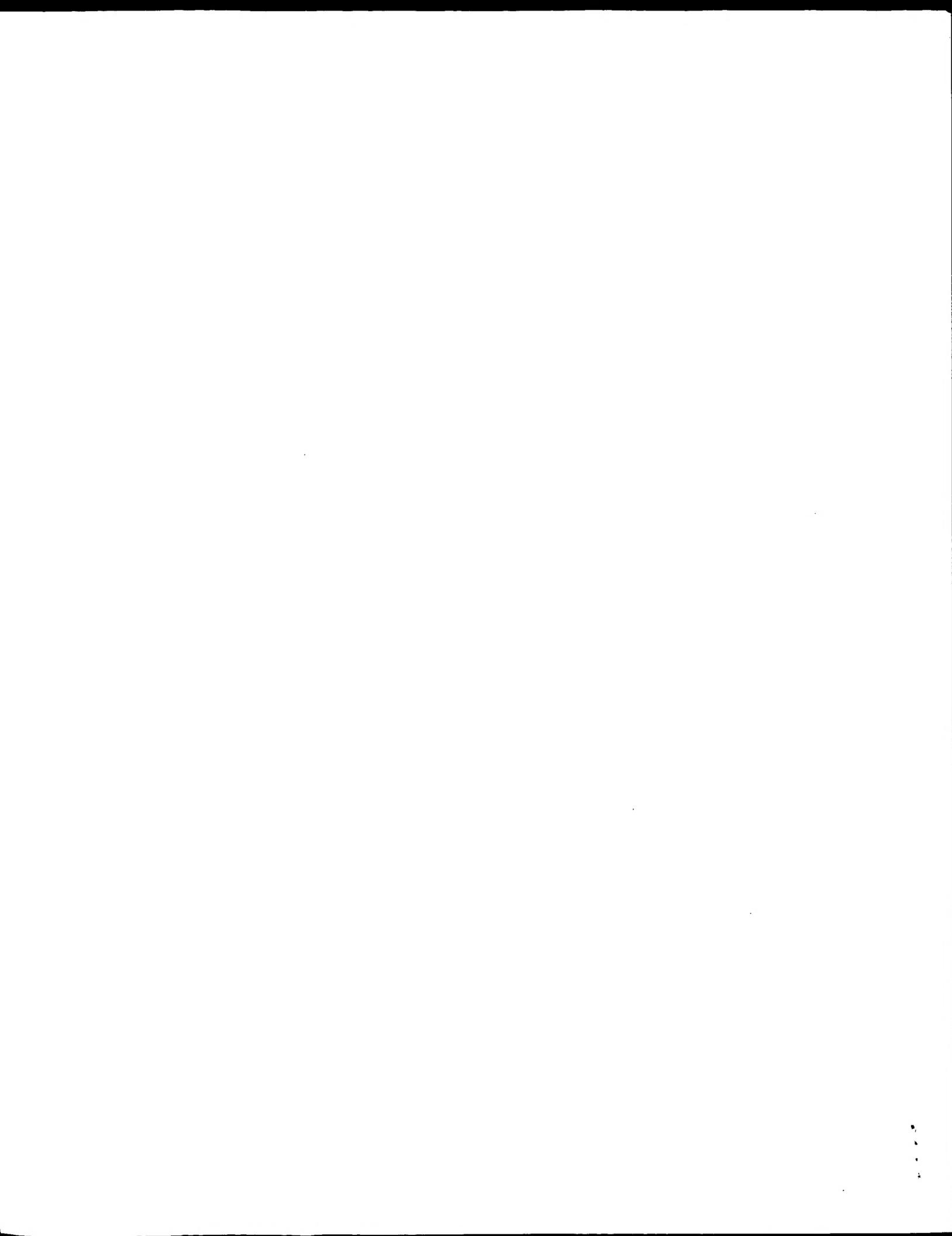
Query Match 4: Score 17.4%; DB 2; Length 349;

Best Local Similarity 27.8%; Pred. No. 3.3e-05;  
 Matches 42; Conservative 17; Mismatches 54; Indels 38; Gaps 8;

Qy 4 CPQGKYIHPQNNSICCTKCHGTYLYNDCPGQQDDCREEGSFTTASNNHLRHCLSCS 63

Db 32 CKDTEY--KRHNLCCLSCCPPTYASRLCDSK-TNTQCTCGSGFTTSNNHHLPAULSCN 87

Qy 64 -KCRKEMGQEVISSCTVDRDTVGCRKNOVRHYWSENLFQCF----NC5LCLNGTVHLS 117



Result No.	Score	Query Match	Length	DB ID	Description
1	941	100.0	455	1 TR1A_HUMAN	P19438 homo sapien
2	716.5	76.1	461	1 TR1A_FIG	P50555 sus scrofa
3	680	72.3	454	1 TR1A_MOUSE	P25118 mus musculus
4	674.5	71.7	471	1 TR1A_BOVIN	O19131 bos taurus
5	669	71.1	461	1 TR1A_RAT	P23934 rattus norvegicus
6	200.5	21.3	176	1 TR23_MOUSE	Q93138 mus musculus
7	200.5	21.3	417	1 TR12_HUMAN	Q93138 h tumor necrosis factor receptor type I
8	198.5	21.1	180	1 TR22_MOUSE	Q9ee62 mus musculus
9	19.5	19.9	435	1 TR13_HUMAN	P36941 homo sapien
10	182.5	19.4	427	1 TR16_HUMAN	P09138 homo sapien
11	181.5	19.3	417	1 TR16_MOUSE	Q920W1 mus musculus
12	181	19.2	474	1 TR1B_MOUSE	P25119 mus musculus
13	179.5	19.1	326	1 VT2_MYXV	P29825 myxoma virus
14	178	18.9	325	1 VT2_SFVKV	P25943 shope fibroma virus
15	176.5	18.8	332	1 TNR6_PIG	O77736 sus scrofa
16	176.5	18.8	425	1 TR16_RAT	P07174 rattus norvegicus
17	167.5	17.8	289	1 TNR5_MOUSE	P27512 mus musculus
18	167.5	17.8	415	1 TNR3_MOUSE	P08448 mus musculus
19	167	17.7	269	1 TNR5_BOVIN	P28203 bos taurus
20	166.5	17.7	323	1 TNR6_BOVIN	P51677 bos taurus
21	166.5	17.7	349	1 CRMB_CAMPY	Q8UYA7 camelpox virus
22	164	17.4	349	1 CRMB_VARY	P34015 variova virus
23	164	17.4	351	1 CRMB_COMPX	O73559 cowpox virus
24	164	17.4	401	1 T11B_HUMAN	P00300 homo sapiens
25	162.5	17.3	327	1 TNR6_MOUSE	P25446 mus musculus
26	161	17.1	461	1 TR1B_HUMAN	P03333 homo sapiens
27	156	16.8	401	1 T11B_RAT	O88727 rattus norvegicus
28	154	16.4	401	1 T11B_MOUSE	O88712 mus musculus
29	147	15.6	324	1 TNR6_RAT	Q63199 rattus norvegicus
30	145	15.4	416	1 TR16_CHICK	P18519 gallus gallus
31	142	15.1	283	1 TR14_HUMAN	Q22956 homo sapiens
32	142	15.1	386	1 T10D_HUMAN	Qubin6 homo sapiens
33	141	15.0	1680	1 FUR2_DRONE	P30432 drosophila

Scoring table: BLOSUM62  
GapOp 10.0 , Gapext 0.5  
Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : SwissProt\_40.4\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  
[1] - RN [1] - RN

## SUMMARIES

RESULT 1  
TR1A\_HUMAN  
ID TR1A\_HUMAN  
AC P19438;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE Tumor necrosis factor receptor superfamily member 1A precursor (p60)  
(TNF-R1) (P55) (CD120a) [Contains: Tumor necrosis factor binding protein 1 (TBPI)].  
GN TNFRSF1A OR TNFA OR TNFR.  
OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_Taxid=9606;  
RN [1] - RN  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=90235285; PubMed=2158863;  
RA Schall T.J., Lewis M., Koller K.J., Lee A., Rice G.C., Wong G.H.W., Granger G.A., Lentz R., Raab H., Kohl W.J., Goeddel D.V.;  
RA "Molecular cloning and expression of a receptor for human tumor necrosis factor";  
RT necrosis factor; [2]  
RN Cell 61:361-370(1990).  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90135284; PubMed=2158862;  
RA Loetscher H., Pan Y.-C.E., Lahm H.-W., Gentz R., Brockhaus M., Tabuchi H., Lesslauer W.;  
RT "Molecular cloning and expression of the human 55 kd tumor necrosis factor receptor";  
RT factor receptor; [3]  
RN Cell 61:351-359(1990).  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 41-53; 110-124 AND 199-201.  
RX MEDLINE=91006021; PubMed=1698610;  
RA Nophar Y., Kemper O., Brakke C., Engelmann H., Zwang R., Aderka D., Hollmann H., Wallach D.;  
RA "Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the type I TNF-R, cloned using amino acid sequence data of its soluble form, encodes both the cell surface and a soluble form of the receptor";  
RT receptor; [4]  
RN EMBO J. 9:3269-3278(1990).  
RP SEQUENCE FROM N.A.  
RX Himmer A., Maurer-Poggy I., Kroenke M., Scheurich P., Pfizenmaier K., Lantz M., Olsson I., Hauptmann R., Stratowa C., Adolf G.R.;  
RA "Molecular cloning and expression of human and rat tumor necrosis factor receptor chain (p60) and its soluble derivative, tumor necrosis factor-binding protein";  
RT DNA Cell Biol. 9:705-715(1990).  
RN SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=91017559; PubMed=2170974;  
RA Gray P.W., Barrett K., Chantzy D., Turner M., Feldman M.;

RT "Cloning of human tumor necrosis factor (TNF) receptor cDNA and  
expression of recombinant soluble TNF-binding protein.";  
RL PROC. Natl. Acad. Sci. U.S.A. 87:7380-7384(1990).  
RN [6]

SEQUENCE FROM N.A.  
RN MEDLINE=92250049; PubMed=1315717;  
RA Fuchs P., Serehl S., Dworzak M., Himmeler A., Ambros P.F.;  
RT "structure of the human TNF receptor 1 (p60) gene (TNFR1) and  
localization to chromosome 12p13.;"  
RL Genomics 13:219-224 (1992).  
RN [8]

SEQUENCE FROM N.A.  
RN TISSUE=muscle;  
RA Strasberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [9]

SEQUENCE OF 41-45.  
RN MEDLINE=90110215; PubMed=2153136;  
RA Engelmann H., Novick D., Wallach D.;  
RT "Two tumor necrosis factor-binding proteins purified from human  
urine. Evidence for immunological cross-reactivity with cell surface  
tumor necrosis factor receptors.";  
RL Biol. Chem. 265:1531-1536(1990).

X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 30-211 IN COMPLEX WITH TNFB.  
RN MEDLINE=93228809; PubMed=8387891;  
RA Baumer D.W., D'Arcy A., James W., Gentz R., Schoenfeld H.-J.,  
RA Briger C., Loetscher H., Lesslauer W.;  
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF  
beta complex: implications for TNF receptor activation.";  
RL Cell 73:431-445(1993).  
RN [10]

X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS) OF 41-202.  
RN MEDLINE=97094982; PubMed=8939750;  
RA Naismith J.H., Devine T.Q., Khono H., Sprang S.R.;  
RT "Structures of the extracellular domain of the type I tumor necrosis  
factor receptor";  
RL Structure 4:1251-1262(1996).  
RN [11]

VARIANTS PHF ARG-9; TYR-62; MET-79; PHE-81; ARG-117 AND TYR-117.  
RN MEDLINE=99213501; PubMed=10199409;  
RA McDermott M.F., Aszkenasy Jevich T., Galon J., McDermott E.M.,  
OGunkolade B.W., Centola M., Mansfield E., Gadina M., Kerenko L.,  
Petterson T., McCarthy J., Frucht D.M., Aringer M., Torosyan Y.,  
Teppo A.-M., Wilson S.M., Kararslan H.M., Wan Y., Todd I., Wood G.,  
Schlimgen R., Kummarajeewa T.R., Cooper S.M., Vella J.P., Amos C.I.,  
Mulley J., Quane K.A., Molloy M.G., Ruakia A., Powell R.J.,  
RA Hitman G.A., O'Shea J., Kastner D.L.;  
RT "Germline mutations in the extracellular domains of the 55 kda TNF  
receptor, TNFR1, define a family of dominantly inherited  
autoinflammatory syndromes.;"  
RL Cell 97:133-144(1999).

-!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
CC TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits  
CC caspase-8 to the activated receptor. The resulting death-inducing  
CC signaling complex (DISC) performs caspase-8 proteolytic activation  
CC which initiates the subsequent cascade of caspases (aspartate-  
CC specific cysteine proteases) mediating apoptosis. Contributes to  
CC the induction of noncytoidal TNF effects including anti-viral  
CC state and activation of the acid sphingomyelinase.  
CC -!- SUBUNIT: TNF binding to the extracellular domain of TNFR1 leads to  
CC homotrimerization. Once aggregated the receptors death domains  
CC provide a novel molecular interface that interacts specifically  
CC with the death domain of TRADD. Various trans-interacting  
CC proteins such as TRAF, RIP and possibly FADD, are recruited to  
CC TNFR complex by their association with TRADD. This complex  
CC activates at least two distinct signaling cascades, apoptosis and  
CC NF-kappa B signaling.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.  
CC -!- DOMAIN: THE DOMAIN THAT INDUCES A-SMASE IS PROBABLY IDENTICAL TO  
THE DEATH DOMAIN THE N-SMASE ACTIVATION DOMAIN (NSD) IS BOTH  
NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
CC NECESSARY AND SUFFICIENT FOR ACTIVATION OF N-SMASE.  
CC PTM: The soluble form is produced from the membrane form by

---

CC proteolytic processing.  
CC -!- DISEASE: Defects in TNFRSF1A are a cause of autosomal dominant  
CC familial hibernian fever (FHF), a disease characterized by  
CC recurrent fever, abdominal pain, localized tender skin lesions and  
myalgia.  
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
CC -!- DATABASE: NAME=PRO; NOTE=CD guide CD120a entry;  
RT WWW="http://www.ncbi.nlm.nih.gov/procd/cd120a.htm".  
RN [12]

This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial/  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC DR EMBL; X53313; CAA39021.1; -.  
CC DR EMBL; M3229; AAA03210.1; -.  
CC DR EMBL; M8286; AAA6753.1; -.  
CC DR EMBL; M6121; AAA6754.1; -.  
CC DR EMBL; M75866; AAA61201.1; -.  
CC DR EMBL; M75864; AAA61201.1; JOINED.  
CC DR EMBL; M75865; AAA61201.1; JOINED.  
CC DR EMBL; M60275; AAA36756.1; -.  
CC DR EMBL; A21522; CAA01558.1; -.  
CC DR EMBL; BC010140; AAH10140.1; -.  
CC DR PIR; A34899; GC0HII.  
CC DR PIR; A35010; A35010.  
CC DR PIR; S12057; S12057.  
CC DR PIR; A38208; A38208.  
CC DR PDB; 1INR; 31-JUL-94.  
CC DR PDB; 1NCF; 07-DEC-95.  
CC DR PDB; 1EXT; 11-JAN-97.  
CC DR Gene; HGNC:11916; TNFRSF1A.  
CC DR MIM; 191190; -.  
CC DR InterPro; IPR00488; Death.  
CC DR InterPro; IPR001368; TNFR\_c6.  
CC DR Pfam; PF00020; TNFR\_c6; 4.  
CC DR Pfam; PF00531; death; 1.  
CC DR SMART; SM00005; DEATH; 1.  
CC DR SMART; SM00248; TNFR.  
CC DR PROSITE; PS00522; TNFR\_NGFR\_1; 3.  
CC DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
CC DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
CC KW Disease mutation; Polymorphism; Repeat; Signal;  
KW SIGNAL 1 21  
FT SIGNAL 22 455 TUMOR NECROSIS FACTOR RECEPTOR  
FT CHAIN 41 291 SUPERFAMILY MEMBER 1A, MEMBRANE FORM.  
FT DOMAIN 22 211 TUMOR NECROSIS FACTOR BINDING PROTEIN 1.  
FT TRANSMEM 212 234 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 235 455 POTENTIAL.  
FT DOMAIN 43 82 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 83 125 TNFR-CYS 1.  
FT REPEAT 126 166 TNFR-CYS 2.  
FT REPEAT 167 196 TNFR-CYS 3.  
FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DISUFD 355 441 DEATH.  
FT DISUFD 44 58  
FT DISUFD 59 72  
FT DISUFD 167 196 TNFR-CYS 4.  
FT DOMAIN 338 348 N-SMASE ACTIVATION DOMAIN (NSD).  
FT DISUFD 102 117  
FT DISUFD 105 125  
FT DISUFD 127 143  
FT DISUFD 146 158  
FT DISUFD 149 166  
FT DISUFD 168 179

Query Match	100.0%	Score 941; DB 1; Length 455;
Best Local Similarity	100.0%	Pred. No. 1.2e-71; Mismatches 0; Indels 0; Gaps 0;
Matches 161; Conservative	0	
Qy 1	DSVCPGKTHPQNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENLRHCL 60	
Db 41	DSVCPGKTHPQNNISICCTKCHGTLYNDCPGRQDFTCREEGSFTASSENLRHCL 100	
DR	SMART; SM00005; DEATH; 1.	
DR	SMART; SM00208; TNFR; 3.	
DR	PROSITE; PS00652; TNFR_NGR_1; 3.	
DR	PROSITE; PS00505; TNFR_NGR_2; 2.	
DR	PROSITE; PS00517; DEATH_DOMAIN_1.	
KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.	
FT SIGNAL	1	21 POTENTIAL.
FT CHAIN	22	461 TUMOR NECROSIS FACTOR RECEPTOR SUPERAMILY MEMBER 1A.
FT DOMAIN	22	210 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	211	233 CYTOPASMIC (POTENTIAL).
FT DOMAIN	234	461 TNFR_CTS_1.
FT REPEAT	43	82 TNFR_CYS_2.
FT REPEAT	83	125 TNFR_CYS_3.
FT REPEAT	126	166 N-SMAB ACTIVATION DOMAIN (NSD).
FT DOMAIN	167	195 DEATH.
FT DOMAIN	340	350
FT DISULFID	447	
FT DISULFID	44	58 BY SIMILARITY.
FT DISULFID	59	72 BY SIMILARITY.
FT DISULFID	81	81 BY SIMILARITY.
FT DISULFID	84	99 BY SIMILARITY.
FT DISULFID	102	117 BY SIMILARITY.
FT DISULFID	105	125 BY SIMILARITY.
FT DISULFID	127	143 BY SIMILARITY.
FT DISULFID	146	158 BY SIMILARITY.
FT DISULFID	149	166 BY SIMILARITY.
FT DISULFID	168	179 BY SIMILARITY.
FT DISULFID	182	194 BY SIMILARITY.
FT DISULFID	185	190 BY SIMILARITY.
FT CARBOHYD	54	54 N-LINKED (GLCNAC, . .) (POTENTIAL).
FT CARBOHYD	86	86 N-LINKED (GLCNAC, . .) (POTENTIAL).
FT CARBOHYD	145	145 N-LINKED (GLCNAC, . .) (POTENTIAL).
FT CARBOHYD	151	151 N-LINKED (GLCNAC, . .) (POTENTIAL).
SEQUENCE	461 AA;	50696 MW; CD72361EC60CD43 CRC64;
Query Match	76.1%; Score 716.5; DB 1; Length 461;	
Best Local Similarity	77.4%; Pred. No. 5.8e-53;	
Matches 120; Conservative 12; Mismatches 22; Indels 1; Gaps 1;		
Gene ID	TRIA_MOUSE	STANDARD;
AC	P25118;	PRT;
DR	01-MAY-1992 (Rel. 22, Created)	
DR	01-MAY-1992 (Rel. 22, Last sequence update)	
DR	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)	
DE	Tumor necrosis factor receptor superfamily member 1A precursor (p60)	
DE	(TNF-RI) (p55)	
GN	TNFRSF1A OR TNFR1.	
OS	Sus scrofa (PIG)	
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
OC	Mammalia; Eutheria; Cetartiodactyla; Sina; Suidae; Sus.	
NCBI_TaxID	9823; [1]	
RN	RP	
SEQUENCE FROM N.A.		
RC	SEQUENCE=Kidney;	
RX	MEDLINE=96011645; PubMed=7590278;	
Sutur B., Pauli U.H.; RT	"Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor".	
RT receptor"; RL	Gene 163:263-266 (1995).	
CC	-!- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (asparagine-specific cysteine proteases) mediating apoptosis (BY SIMILARITY).	
CC	-!- SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO HOMOPRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING PROTEINS SUCH AS TRAF5, RIP AND POSSIBLY FADD, ARE RECRUITED TO TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).	
CC	-!- SIMILARITY: Type I member protein.	
CC	-!- SIMILARITY: Contains 4 TNFR-CYS REPEATS.	
CC	-!- SIMILARITY: Contains 1 DEATH DOMAIN.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
EMBL; U19994; AAC48499.1; -		
HSSP; P19438; 1TNTR.		
InterPro; IPR000498; Death.		
InterPro; IPR001368; TNFR_C6.		
PFam; PF00020; TNFR_C6; 3.		
PFam; PF00531; death; 1.		
Prodrom; PD000771; TNFR_C6; 1.		
DR	SEQUENCE FROM N.A.	
RP	MEDLINE=9118785; PubMed=1842278;	
RX	Lewis M., Tricoglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.,	
RA	"Cloning and expression of cDNAs for two distinct murine tumor	
RA	RT	

RT necrosis factor receptors demonstrate one receptor is species specific.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:91246168; PubMed=1645445;  
 RA Goodwin R.G., Anderson D., Jerry R., Davis T., Brannan C.I.,  
 RA Copeland N.G., Jenkins N.A., Smith C.A.;  
 RT "Molecular cloning and expression of the type 1 and type 2 murine  
 RT receptors for tumor necrosis factor.";  
 RL Mol. Cell. Biol. 11:3050-3026(1991).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:9128014; PubMed=1647956;  
 RA Barrett K., Taylor-Fishwick D.A., Cope A.P., Kissnerghis A.M.,  
 RA Gray P.W., Feldmann M., Foxwell B.M.J.; analysis of the murine p55  
 RT "Cloning, expression and cross-linking of tumor necrosis factor receptor.";  
 RL Eur. J. Immunol. 21:1649-1656(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE:9203815; PubMed=1657766;  
 RA Rothe J.G., Brockhaus M., Gentz R., Lesslauer W.;  
 RT "Molecular cloning and expression of the mouse Tnf receptor type b.";  
 RL Immunogenetics 34:1338-1340(1991).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:9424292; PubMed=8108324;  
 RA Bebo B.F., Lintilicau D.S.,  
 RT "Nucleotide sequence of the TNF type I receptor from a mouse  
 endochelioma cell line.";  
 RL Immunogenetics 39:450-451(1994).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE:93156721; PubMed=8301516;  
 RA Rothe J., Bluthmann H., Gentz R., Lesslauer W., Steinmetz M.;  
 RT "Genomic organization and promoter function of the murine tumor  
 necrosis factor receptor beta gene.";  
 RL Mol. Immunol. 30:165-175(1993).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Strasberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 CC !- FUNCTION: Receptor for TNFSF2/TNF-alpha and homotrimeric  
 TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits  
 RT caspase-8 to the activated receptor. The resulting death-inducing  
 CC caspase-8 to the activated receptor. The resulting death-inducing  
 CC signaling complex (DISC) performs caspase-8 proteolytic activation  
 CC which initiates the subsequent cascade of caspases (aspartate-  
 CC specific cysteine proteases) mediating apoptosis (By similarity).  
 CC SUBUNIT: TNF BINDING TO THE EXTRACELLULAR DOMAIN OF TNFR1 LEADS TO  
 CC HOMOTRIMERIZATION. ONCE AGGREGATED THE RECEPTORS DEATH DOMAINS  
 CC PROVIDE A NOVEL MOLECULAR INTERFACE THAT INTERACTS SPECIFICALLY  
 CC WITH THE DEATH DOMAIN OF TRADD. VARIOUS TRADD-INTERACTING  
 PROTEINS SUCH AS TRAF, RIP AND POSSIBLY FADD, ARE RECRUITED TO  
 TNFR1 COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX  
 ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND  
 CC NF-KAPPA B ACTIVATION (BY SIMILARITY).  
 CC !- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC !- SIMILARITY: CONTAINS 4 TNFR-CVS REPEATS.  
 CC !- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to licensee@isb-sib.ch).

DR EMBL; X57796; CA040936 1; -.  
 DR EMBL; I26349; AAA59361.1; -.  
 DR EMBL; MT6656; AAA0465.1; -.  
 DR EMBL; MB8067; AAA0465.1; JOINED.  
 DR EMBL; M6655; AAA0465.1; JOINED.  
 DR EMBL; BC004539; AAH04599.1; -.  
 DR PIR; A38634; GQMSLT.  
 DR PIR; S16677; S16677.  
 DR PIR; S19021; S19021.  
 DR HSSP; PI9438; IEXT.  
 DR MGD; MGI:1314884; Trfksfla.  
 DR InterPro; IPR0048; Death.  
 DR Pfam; PF00020; TNFR\_c6.  
 DR Pfam; PF00531; death\_1.  
 DR ProDom; PD00071; TNFR\_c6\_1.  
 DR SMART; SM0005; DEATH\_1.  
 DR SMART; SM0208; TNFR\_NGFR\_1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2.  
 DR PROSITE; PS50017; DEATH\_DOMAIN\_1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 454 TUMOR NECROSIS FACTOR RECEPTOR  
 FT DOMAIN 22 212 SUPERFAMILY MEMBER 1A.  
 FT TRANSMEM 213 235 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 236 454 POTENTIAL.  
 FT REPEAT 43 82 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 83 125 TNFR-CYS 1.  
 FT REPEAT 126 166 TNFR-CYS 2.  
 FT REPEAT 167 196 TNFR-CYS 3.  
 FT DOMAIN 339 349 TNFR-CYS 4.  
 FT DOMAIN 356 441 N-SMASE ACTIVATION DOMAIN (NSD).  
 FT DISURFID 44 58 DEATH.  
 FT DISURFID 59 72 BY SIMILARITY.  
 FT DISURFID 62 81 BY SIMILARITY.  
 FT DISURFID 84 99 BY SIMILARITY.  
 FT DISURFID 102 117 BY SIMILARITY.  
 FT DISURFID 105 125 BY SIMILARITY.  
 FT DISURFID 127 143 BY SIMILARITY.  
 FT DISURFID 146 158 BY SIMILARITY.  
 FT DISURFID 149 166 BY SIMILARITY.  
 FT DISURFID 168 179 BY SIMILARITY.  
 FT DISURFID 182 195 BY SIMILARITY.  
 FT DISURFID 185 191 BY SIMILARITY.  
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 394 394 R -> G (IN REF. 6).  
 SQ SEQUENCE 454 AA; 50129 MW; 071028B3C2B6D9 CRC64;

Query Match 72.3%; Score 680; DB 1; Length 454;  
 Best Local Similarity 71.3%; Pred No. 6; 2e-50; Indels 0; Gaps 0;  
 Matches 112; Conservative 19; Mismatches 26; Index 0;

Qy 1 DSVCPGKVKIHPQNSICCTKCHGTYLNDPGPQDTPCRECESGFTASENHLRCL 60  
 Db 41 DSCLPQGKVHKSKNSICCTKCHGTYLVSDCPSPGRDTVCRECKGFTASQNLQCL 100

Qy 61 SOSKRKEMQVQEVSCTVDRDYVGCRKQYRHWSNLQCFNCSCILNLGVHLSQEB 120  
 Db 101 SCKTCRKEMQVQEVSQPCQADKDPYGCKENQFOLSYSTFHFCVDCPCFNGTVTIPCKE 160

Qy 121 KONTVTCGHAGFFLRENECNSCNSKKSLCTKCHGTYLVSDCPSPGRDTVCRECKGFTASQNLQCL 157

Db 161 TQNTVCNCHAGFFLRESECVPCSHCKNNBECMKLCLP 197

RESULT 4  
 TRIA\_BOVIN TRIA\_BOVIN STANDARD PRT; 471 AA.  
 ID TRIA\_BOVIN  
 AC 019131;



CC	TNFR COMPLEX BY THEIR ASSOCIATION WITH TRADD. THIS COMPLEX ACTIVATES AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING (BY SIMILARITY).
CC	-!- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC	-!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC	-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	ENTREZ: M63122; AAH42255_1; -
DR	EMBL: AF329976; ARK53562_1; -
DR	EMBL: AF329977; ARK53563_1; -
DR	EMBL: AF329978; ARK53567_1; -
DR	EMBL: AF329978; ARK53569_1; -
DR	EMBL: AF329979; ARK53565_1; -
DR	EMBL: AF329980; ARK53566_1; -
DR	PIR: B35555; B36555;
DR	HSPB; P39438; INCR;
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00020; TNFR_c6_4.
DR	ProDom; PD000771; TNFR_c6_1.
DR	SMART; SM0005; DEATH_1.
DR	SMART; SM0028; TNFR_3.
DR	PROSITE; PS00652; TNFR_NGFR_1; 3.
DR	PROSITE; PS00505; TNFR_NGFR_2; 3.
DR	PROSITE; PS0017; DEATH_DOMAIN_1.
KW	Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
FT	SIGNAL_1
FT	CHAIN_22
FT	461 TUMOR_NECROSIS_FACTOR_RECEPATOR_SUPERFAMILY_MEMBER_1A.
FT	DOMAIN_22 EXTRACELLULAR_(POTENTIAL).
FT	TRANSMEM_212 POTENTIAL.
FT	DOMAIN_235 CYTOPLASMIC_(POTENTIAL).
FT	REPEAT_43 TNFR-CYS_1.
FT	REPEAT_83 TNFR-CYS_2.
FT	REPEAT_126 TNFR-CYS_3.
FT	REPEAT_167 TNFR-CYS_4.
FT	DOMAIN_344 N-SMASE_ACTIVATION_DOMAIN_(NSD).
FT	DOMAIN_363 DEATH.
FT	DISULPID_44 BY_SIMILARITY.
FT	DISULPID_59 BY_SIMILARITY.
FT	DISULPID_62 BY_SIMILARITY.
FT	DISULPID_84 BY_SIMILARITY.
FT	DISULPID_102 BY_SIMILARITY.
FT	DISULPID_105 BY_SIMILARITY.
FT	DISULPID_127 BY_SIMILARITY.
FT	DISULPID_146 BY_SIMILARITY.
FT	DISULPID_149 BY_SIMILARITY.
FT	DISULPID_168 BY_SIMILARITY.
FT	DISULPID_179 BY_SIMILARITY.
FT	DISULPID_182 BY_SIMILARITY.
FT	DISULPID_185 BY_SIMILARITY.
FT	CARBONYD_154 N-LINKED(GLCNAC_.) (POTENTIAL).
FT	CARBONYD_151 N-LINKED(GLCNAC_.) (POTENTIAL).
FT	CARBONYD_201 N-LINKED(GLCNAC_.) (POTENTIAL).
FT	VARIANT_230 I->V (IN STRAINS LEW_NHSD, ACI/SEGHSND, DA/BKL AND F34/NHSD).
FT	VARIANT_295 H->P (IN STRAINS LEW_NHSD, ACI/SEGHSND, DA/BKL, F34/NHSD AND BN/SSNHSD).
SQ	SEQUENCE_461 AA: 50969 MW: EB23C05450FB202 CRC64;
QY	Query Match 71.1%; Score 669; DB 1; Length 461; Best Local Similarity 68.3%; Pred. No. 5.2e-49; Matches 110; Conservative 18; Mismatches 33; Indels 0; Gaps 0;
QY	1 DSVCPQGKYTHQDNNSICCTKCHGTYLYNDCPGPQGDTCRCESGSFTASENHLRHCL 60
Db	41 DNLSQPQGXAHPRANSTCCTKCHGTYLYNDCPGPQGDTCRCESGSFTASENHLRHCL 100
Qy	61 SCCRCKENGQVEISSCTVDRDVCGCRKQYRHYNSENLQCFNCNLSCINGTVHLSQE 120
Db	101 SCKTRKEMQVETSPKADMDTVCGGKKNQFORYLSETHQCVDCSPCFCNGTIVPK 160
Qy	121 KQNVTCGHAGFLRENCVSNCNSKSLETKLCPOIEN 161
Db	161 KQNTVCNCHAGFFLGSNBCTPCSHCKNQECMKLCLPPVAN 201
RESULT 6	
ID	TR23_MOUSE
ID	TR23_MOUSE STANDARD; PRT; 176 AA.
AC	Q9E663; Q8VHQ0; -
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Tumor necrosis factor receptor superfamily member 23 (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB).
GN	TNFRSF23 OR TNFRSF11B OR TNFRHL.
OS	Mus musculus (Mouse)
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1] RA
RN	SEQUENCE FROM N.A.
RX	STRAIN=29/SV; TISSUE=Embryonic stem cells;
RX	MEDLINE=20516229; PubMed=11063788;
RX	Engemann S., Stroodtke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.,
RX	"Sequence and functional implications for a novel imprinting centre and extended imprinting.";
RL	Hum. Mol. Genet. 9:2691-2706(2000).
RN	[2] RA
RN	SEQUENCE FROM N.A.
RA	Pan G., Mao W., Risser P.; "Characterization of SOB, a member of the TNFR family." Submitted (JUL-2001) to the EMBL/Genbank/DDBJ databases.
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC	-!- TISSUE SPECIFICITY: ubiquitous.
CC	-!- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
DR	EMBL: AJ778264; CAC16405_1; -
DR	EMBL: AJ776515; CAC27352_1; -
DR	HSSP; P19438; 1EXT.
DR	MGI; MGI-1930269; TNfrsf23.
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00020; TNFR_c6_3.
DR	SMART; SM0028; TNFR_3.
DR	PROSITE; PS00505; TNFR_NGFR_2; 2.
KW	Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.
FT	DOMAIN_1 9 CYTOPLASMIC_(POTENTIAL); SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT	TRANSMEM_10 30 (POTENTIAL).
FT	DOMAIN_31 176 EXTRACELLULAR_(POTENTIAL).
FT	REPEAT_37 72 TNFR-CYS_1.
FT	REPEAT_74 114 TNFR-CYS_2.
FT	REPEAT_115 155 TNFR-CYS_3.
FT	DISULPID_38 49 BY_SIMILARITY.
FT	DISULPID_50 63 BY_SIMILARITY.
FT	DISULPID_53 72 BY_SIMILARITY.
FT	DISULPID_75 90 BY_SIMILARITY.

FT	DISULFID	93	106	BY SIMILARITY.	
FT	DISULFID	96	114	BY SIMILARITY.	
FT	DISULFID	116	131	BY SIMILARITY.	
FT	DISULFID	134	147	BY SIMILARITY.	
FT	DISULFID	137	155	BY SIMILARITY.	
FT	CARBOHID	148	148	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SC	SEQUENCE	176 AA;	19594 MW:	EE30D617949DBB7 CRC64;	
Query Match		21.3%	Score 20.5; DB 1; Length 176;		
Best Local Matches	2; Conservative	33.8%; Pred. No. 2.4e-10;			
Matches	16; Mismatches	60; Indels	7; Gaps	4;	
Qy	4 CPQKYTHPQNSICCTKCHKGTYLYNDCPGQDTCRECBGSFTASENHLRHCLSCS	63			RL Curr. Biol. 6:1669-1676 (1996). [5]
Db	38 CPDGEX--QSNDVCKTKPSGTFVAKPKLPHQSQCBEQCRPEFTGKDNGHDCELCS	94			RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7; 8; 9 AND 10).
Qy	64 KORKENGQVEISCTYDRDTYVGCRKNQYRHYWSNLFCQFNCSLCLNG-TVHLSQEQKQ	122			RP MEDLINE=972/7273; PubMed=914039;
Db	95 TCDKDNMV-.ADCSATSDRKCECQIGLY-YDPKFPESCRPCKCPQSIQPVNLQECNSTA	151			RX Screamton G.R., Xu X.-N., Olsen A.L., Cowper A.E., Tan R., RA McMichael A.J., Bell J.I.;
Qy	123 NTVCST 127				RT "LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing."
Db	152 NTVCVS 156				RT PROC. Natl. Acad. Sci. U.S.A. 94:4615-4619(1997).
RESULT 7					RL RN [6];
TR12_HUMAN					RN SEQUENCE FROM N.A. (ISOFORMS 11 AND 12).
ID	Tumor necrosis factor superfamily member 12 precursor	PRT; 417 AA.			RP MEDLINE=98113360; PubMed=9446802.
AC	Q93036; Q93337; Q92983; P78515; Q99722; P78507;				RX RA Warzocha K., Ribiero P., Charlot C., Renard N., Coiffier B., RA Salles G.;
AC	Q99830; Q9BY86; O14865; O14866; O00275; O00277; O00278;				RA RT "A new death receptor 3 isoform: expression in human lymphoid cell lines and non-Hodgkin's lymphomas,"
AC	O00280; Q9UNEO; Q9UME5; Q9ME5;				RN RA RP SEQUENCE FROM N.A. (ISOFORM 1).
DT	01-NOV-1997 (Rel. 35, Created)				RA RA Shiozawa S., Konishi Y., Murayama K., Mukae N., Yamamoto E., RA Hayashi S., Sato M., Shiozawa K., Tsukamoto Y.;
DT	01-NOV-1997 (Rel. 35, Last sequence update)				RA RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DT	15-JUN-2002 (Rel. 41, Last annotation update)				RA RN [8];
DE	Tumor necrosis factor receptor superfamily member 12 precursor (WSL-1 protein) (Apoptosis-mediating receptor DR3) (Apoptosis-mediating receptor TRAMP) (Death domain receptor 3) (WSL protein)				RP RP SEQUENCE OF 4-417 FROM N.A.
DE	(Apoptosis inducing receptor AIR) (Apo-3) (Lymphocyte associated receptor of death) (LARD).				RC RC TISSUE=Brain, and Peritoneal;
GN	TNFRSF12 OR WSL1 OR WSL OR APO3 OR DR3 OR DDR3.				RA RA Chaudhary P.M., Hood L.E.;
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Homidae; Homo.				RA RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
OC					CC CC "- FUNCTION: Receptor for TNFSF12/APO3/TWEAK. Interacts directly with the adaptor TRADD. Mediates activation of NF-kappaB and induces apoptosis. May play a role in regulating lymphocyte homeostasis.
OX					CC CC "- SUBUNIT: HOMODIMER. INTERACTS STRONGLY VIA THE DEATH DOMAINS WITH THE TNFR1-ASSOCIATED MOLECULE TRADD AND THE TNRF1 RECEPTOR TO ACTIVATE AT LEAST TWO DISTINCT SIGNALING CASCADES, APOPTOSIS AND NF-KAPPA B SIGNALING.
RN	[1] NCBI_TaxID=9606;				CC CC "- SUBCELLULAR LOCATION: Type I membrane protein (isoforms 1, 2, 9 and 11); Secreted (isoforms 3, 4, 5, 6, 7, 8, 10 and 12).
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 3 AND 4), AND MUTAGENESIS.				CC CC "- (Potential) CC CC "- ALTERNATIVE PRODUCTS: 12 ISOFORMS; 1/WSL-1/LARD-1A (SHOWN HERE), 2/LARD-1B, 3/WSL-S1/LARD-3, 4/WSL-S2/LARD-2, 5/LARD-4/LARD-11, 6/LARD-5, 7/LARD-6, 8/LARD-7, 9/LARD-8, 10/LARD-9, 11/BETA AND 12/BETA SORRY; ARE PRODUCED BY ALTERNATIVE SPlicing.
RC	SEQUENCE FROM N.A. (ISOFORM 1)				CC CC "- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN THYMOCYTES AND LYMPHOcyTES; DETECTED IN LYMPHOcyTE-RICH TISSUES SUCH AS THYMUS, COLON, INTESTINE, AND SPLEEN. ALSO FOUND IN THE PROSTATE.
RX	Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;				CC CC "- PIM: GLYCOSylATED (PROBABLY).
RA	"A death-domain-containing receptor that mediates apoptosis."				CC CC "- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
RN	[2] RN SEQUENCE FROM N.A. (ISOFORM 1)				CC CC "- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
RP	SEQUENCE FROM N.A. (ISOFORM 1)				CC CC "- CAUTION: Ref. 5 reports for isoform 4 at position 208 a serine residue instead of arginine.
RC	SEQUENCE FROM N.A. (ISOFORM 1)				CC CC "-
RX	Medline=97088617; PubMed=8934525;				This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
RA	Kitson J., Raven T., Jiang Y.-P., Goeddel D.V., Giles K.M., Pun K.-T., Grinham C.J., Brown R., Farrow S.N.;				CC DR EMBL: Y09332; CAA70561.1; -
RX	Medline=97081063; PubMed=8873942;				DR DR EMBL: Y09332; CAA70559.1; -
RA	Chinnaiyan A.M., O'Rourke K., Yu G.-L., Lyons R.H., Garg M., Duan D.R., Xing L., Gentz R., Ni J., Dixit V.M.				DR DR EMBL: Y09332; CAA70560.1; -
RT	"Signal transduction by DR3, a death domain-containing receptor related to TNFR1 and CD95."				DR DR EMBL: U72763; AAC50819.1; -
RN	[3] RN SEQUENCE FROM N.A.				
RP	Degli-Esposti M.A., Din W.S., Cosman D., Smith C.A., Goodwin R.G., Goddard A.D., Bauer K.D., Asikkenzu A.;				
RA	Marsden S.A., Sheridan J.P., Donahue C.J., Pitti R.M., Gray C.L.,				
RA	"Apo-3, a new member of the tumor necrosis factor receptor family, contains a death domain and activates apoptosis and NF-kappa-B.";				

DR EMBL; U83599; AAB41434.1; -.  
 DR EMBL; U83600; AAB41435.1; -.  
 DR EMBL; U78029; AAB40918.1; -.  
 DR EMBL; U747411; AAB3974.1; -.  
 DR EMBL; U94501; AAC51306.1; -.  
 DR EMBL; U94504; AAC51309.1; -.  
 DR EMBL; U94502; AAC51307.1; -.  
 DR EMBL; U94503; AAC51308.1; -.  
 DR EMBL; U94505; AAC51310.1; -.  
 DR EMBL; U94506; AAC51311.1; -.  
 DR EMBL; U94507; AAC51312.1; -.  
 DR EMBL; U94508; AAC51313.1; -.  
 DR EMBL; U94509; AAC51314.1; -.  
 DR EMBL; U94510; AAC51315.1; -.  
 DR EMBL; U94512; AAC51316.1; -.  
 DR EMBL; U83598; AAB4133.1; -.  
 DR EMBL; APO26070; AAC3956.1; -.  
 DR EMBL; APO26071; AAB8228.1; -.  
 DR EMBL; AB051850; BAB40662.1; -.  
 DR EMBL; AB051851; BAB40663.1; -.  
 DR EMBL; U75380; AAC51192.1; -.  
 DR EMBL; U75381; AAC51193.1; -.  
 DR EMBL; U83597; AAB41432.1; -.  
 DR MIM; 603366; -.  
 DR InterPro; IPR000488; Death.  
 DR InterPro; IPR001168; TNFR\_c6.  
 DR Pfam; PF00531; death\_1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 1.  
 DR PROSITE; PS50017; DEATH\_DOMAIN\_1.  
 KW Receptor; Apoptosis; Transmembrane; Alternative splicing; Signal; Repeat; Polymorphism; Signal.

FT SIGNAL 1 24 POTENTIAL.  
 FT CHAIN 25 417 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 12.  
 FT DOMAIN 25 199 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 200 220 POTENTIAL.  
 FT DOMAIN 223 417 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 34 71 TNFR-CYS 1.  
 FT REPEAT 72 115 TNFR-CYS 2.  
 FT REPEAT 116 163 TNFR-CYS 3.  
 FT REPEAT 164 192 TNFR-CYS 4.  
 FT DOMAIN 332 413 DEATH.  
 FT DISULFID 47 49 BY SIMILARITY.  
 FT DISULFID 48 61 BY SIMILARITY.  
 FT DISULFID 51 70 BY SIMILARITY.  
 FT DISULFID 73 89 BY SIMILARITY.  
 FT DISULFID 92 107 BY SIMILARITY.  
 FT DISULFID 95 115 BY SIMILARITY.  
 FT DISULFID 117 130 BY SIMILARITY.  
 FT DISULFID 138 155 BY SIMILARITY.  
 FT DISULFID 141 162 BY SIMILARITY.  
 FT DISULFID 165 176 BY SIMILARITY.  
 FT DISULFID 179 191 BY SIMILARITY.  
 FT DISULFID 187 195 BY SIMILARITY.  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . ) (POTENTIAL).  
 FT VARSPLIC 106 106 MISSING (IN ISOFORM 6, ISOFORM 7 AND  
 FT VARSPLIC 54 98 ISOFORM 9).  
 FT VARSPLIC 156 171 MISSING (IN ISOFORM 8) SRRID:DCGCCLPGFYE -> HPSVTLGORRPHSSTS (IN  
 FT VARSPLIC 172 417 ISOFORM 7) MISSING (IN ISOFORM 7) AND ISOFORM 3).  
 FT VARSPLIC 182 417 MISSING (IN ISOFORM 5 AND ISOFORM 6) STLSGCPCCCAVCGWROM -> PPPSAGAPMGAVOSAVP  
 FT VARSPLIC 182 200 LSVAGGRGV (IN ISOFORM 11).  
 FT VARSPLIC 182 218 STLSGCPCCCAVCGWROMQFWVQVLLLAGIWPILLGA ->  
 FT VARSPLIC 219 417 VLIGCAGPCHGPPPAWGHDPDLHPIPLLASOAPGYCR (IN  
 FT VARSPLIC 182 MISSING (IN ISOFORM 3).  
 FT VARSPLIC 219 417 STLGSCPERCAAVCGWROMFWVQVLLAGIWPILLGATLY  
 FT VARSPLIC 182 277 SASAKI H., Sato K., Schoenbach C., Seya T., Storch K.-F.,

---

RESULT 8 TR22\_MOUSE STANDARD; PRT; 180 AA.  
 ID TR22\_MOUSE\_Q0BZ7; Q0CZAA; Q0VRB9;  
 AC Q0BZ7; Q0CZAA; Q0VRB9;  
 DT 15-JUN-2002 (Rel. 41; Last sequence update)  
 DI 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis factor receptor p50 homolog 2) (TNF receptor family member SOBa).  
 GN TNFRSF22 OR TNFRSF22 OR TNFRH2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/SV; TISSUE:Embryonic stem cells;  
 RX MEDLINE=>2051229; PubMed=11063728;  
 RA Engemann S., Stroedtke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.,  
 RT "Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting";  
 RL Hum. Mol. Genet. 9:2691-2706(2000).  
 RN [2]  
 RA Risser P., Mao W., Baldwin D.T., Pan G.;  
 RA "Characterization of SOBa, a murine member of the TNFR family";  
 RT Submitted (JUL-2001) to the EMBL/Genbank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CE7BL/6J; TISSUE=Embryo;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Akarawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Izawa M., Nishii K., Kyosava H., Kondo S., Yamakawa I.,  
 RA Saito T., Okazaki Y., Gojoh T., Bono H., Kasukawa T., Saito R.,  
 RA Kado K., Matsuda H.A., Ashburner M., Baralov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nakaido T., Pesce G., Quackenbush J.,  
 RA Schriml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarrito P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Storch K.-F.,

RA Suzuki H., Toyo-Oka K., Wang X.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida R., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690 (2001).

CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).  
 CC -|- TISSUE SPECIFICITY: ubiquitous  
 CC -|- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to licensee@isb-sib.ch).

CC DR EMBL; AJ278265; OAC16406\_1; -.  
 DR EMBL; AJ276505; OAC27353\_1; -.  
 DR EMBL; AK046551; AA05073\_1; -.  
 DR EMBL; AK012838; BAB2502\_1; -.  
 DR HSSP; P19438; ITEXT.  
 DR MGI; 1530270; TfNfrsf22.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR SMART; SM00208; TNFR\_3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; Signal-anchor; Transmembrane; Glycoprotein; Repeat.  
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 21 41 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 42 180 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 47 82 TNFR-CYS 1.  
 FT REPEAT 84 124 TNFR-CYS 2.  
 FT REPEAT 125 165 TNFR-CYS 3.  
 FT DISULFID 48 59 BY SIMILARITY.  
 FT DISULFID 60 73 BY SIMILARITY.  
 FT DISULFID 63 82 BY SIMILARITY.  
 FT DISULFID 85 100 BY SIMILARITY.  
 FT DISULFID 103 116 BY SIMILARITY.  
 FT DISULFID 106 124 BY SIMILARITY.  
 FT DISULFID 126 141 BY SIMILARITY.  
 FT DISULFID 144 157 BY SIMILARITY.  
 FT DISULFID 147 165 BY SIMILARITY.  
 FT CARBOYD 62 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 12 12 L->V (IN REF. 3).  
 FT CONFLICT 171 180 RSSASVAPI -> NPNRFLLL (IN REF. 2).  
 SQ SEQUENCE 180 AA; F8F56E165ADD3FA CRC64;

Query Match 21.1%; Score 198 5; DB 1; Length 180;  
 Best Local Similarity 32.8%; Pred. No. 3.6e-10;  
 Matches 41; Conservative 18; Mismatches 59; Indels 7; Gaps 4;

Qy 4 CPQGKTYHPPNNSTCCTKCHKGTYLYNDCPGPQDTDCRECESGSFTASENHLRHCLSCS 63  
 Db 48 CPAGE--WSDVCRNCSAGTVKAPCIPHQGQCSKCHPFTFKDNVYDACTLS 104

Qy 64 KCRKEMGOVEIISCTVDRDTVGCRKNQYRHYSNLFQCFNCSLCNG-TVHLSQEQEKQ 122

Db 105 TCDKD--QENVADCSATSDEKQCRTGLY-YDDPKFPESCRPTKCPQGIPVHQECNSTA 161

Qy 123 NTVCT 127  
 Db 162 NTVCVS 166

RESULT 9  
 TN3\_HUMAN STANDARD PRT; 435 AA.  
 ID TN3\_HUMAN STANDARD PRT; 435 AA.  
 AC P36941; PROSITE; PS00652; TNFR\_NCFR\_1; 2.  
 DT 01-JUN-1994 (Rel. 29, Created) DR PROSITE; PS50050; TNFR\_NCFR\_2; 3.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 30 POTENTIAL.

DT 01-JUN-1994 (Rel. 29, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DB "Tumor necrosis factor receptor superfamily member 3 precursor"  
 DB "(Lymphotoxin-beta receptor)" (Tumor necrosis factor C receptor).  
 DE protein  
 GN LN LTBR OR TNFRSF3 OR TNFCR.  
 OS Homo sapiens (Human).  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBITaxonID=9606;  
 OX RN  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE:9322381; PubMed=8486360;  
 RA Baerts M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.; RT "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";  
 RL Genomics 16:214-218(1993).  
 RN [2].  
 RN SEQUENCE FROM N.A.  
 RC Strausberg R.;  
 RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3].  
 RP FUNCTION.  
 RX MEDLINE:94225209; PubMed=8171323;  
 RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.A.; RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.; RT "A lymphotoxin-beta-specific receptor.";  
 RL Science 264:707-710 (1994).  
 RN [4].  
 RP CHARACTERIZATION.  
 RX MEDLINE:9223511; PubMed=10207006;  
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.; RA "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell death in HeLa cells"; RT J. Biol. Chem. 274:11868-11873 (1999).  
 RN [5].  
 RP FUNCTION.  
 RX MEDLINE:9261554; PubMed=10799510;  
 RA Rooney T.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A., RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.; RT "The lymphocoxin-beta receptor is necessary and sufficient for RT LIGHT-mediated apoptosis of tumor cells.";  
 RL J. Biol. Chem. 275:14307-14315(2000).  
 CC -|- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing LTA and LTb, and for TNFSF4/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs.  
 CC -|- SUBUNIT: Self-associates.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

-----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to licensee@isb-sib.ch).

CC DR EMBL; L04270; AAA36757\_1; -.  
 DR HSSP; P25942; 1CDP.  
 DR Genew; HGNC:6718; LTBR.  
 DR MIM; 600979; -.  
 DR InterPro; IPR01368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6.  
 DR ProdDom; PD000771; TNFR\_C6; 1.  
 DR SMART; SM0208; TNFR\_C6.  
 DR PROSITE; PS00652; TNFR\_NCFR\_1; 2.  
 DR PROSITE; PS50050; TNFR\_NCFR\_2; 3.  
 DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.



Db	141 KQNTVCEBCPDGTYSDLEANHVDPCLPCTVCEDETERQLRECTR	182	FT	DISULFID	37	50	BY SIMILARITY.
RESULT 11			FT	DISULFID	40	57	BY SIMILARITY.
TR16_MOUSE	STANDARD;	PRT;	FT	DISULFID	60	76	BY SIMILARITY.
ID TR16_MOUSE			FT	DISULFID	79	92	BY SIMILARITY.
AC Q920W;			FT	DISULFID	82	100	BY SIMILARITY.
DT 15-JUN-2002 (Rel. 41, Created)			FT	DISULFID	102	115	BY SIMILARITY.
DT 15-JUN-2002 (Rel. 41, Last sequence update)			FT	DISULFID	118	131	BY SIMILARITY.
DT 15-JUN-2002 (Rel. 41, Tumor necrosis factor receptor superfamily member 16 precursor (Low affinity nerve growth factor receptor) (NGF receptor) (Low affinity neurotrophin receptor p75NTR).)			FT	DISULFID	121	139	BY SIMILARITY.
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low affinity nerve growth factor receptor) (NGF receptor) (Low affinity neurotrophin receptor p75NTR).			FT	DISULFID	142	157	BY SIMILARITY.
DB NGFR OR TNFRSF16.			FT	DISULFID	160	173	BY SIMILARITY.
OS Mus musculus (Mouse).			FT	DISULFID	163	181	BY SIMILARITY.
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			FT	CARBOHYD	53	N-LINED	(GLCNAC. . .) (POTENTIAL).
NCBI_TaxID=10050;			SQ SEQUENCE	417 AA:	44686 MW;	5D7A4510DB8AFB2 CRC64;	
RN [1]							
RP STRAIN=N.A.							
RC							
RX MBLINE=9907773; PubMed=9857182;							
RA Tuffereau C., Benejean J., Blondel D., Kieffer B.; Flamand A.;							
RT "Low-affinity nerve-growth factor receptor (p75NTR) can serve as a receptor for rabies virus.";							
RL EMBO J. 17:7250-7259(1998).							
CC -!- FUNCTION: Low affinity receptor which can bind to NGF, BDNF, NT-3, CC neural cells as well as cell death of CC neural cells (By similarity). Binds to rabies virus glycoprotein Gs.							
CC -!- SUBUNIT: Homodimer; disulfide-linked. Interacts with p75NTR- CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).							
CC -!- PTM: N- AND O-Glycosylated (By similarity).							
CC -!- PTM: Phosphorylated on serine residues (By similarity).							
CC -!- SIMILARITY: CONTAINS 4 TNFR CYS REPEATS.							
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.							
CC							
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).							
CC							
EMBL; AF05292; AAD17943; 1. DR HSSP; P07174; INGR.							
DR MGD; MGI:9722; Ngfr.							
InterPro; IPR00488; Death.							
InterPro; IPR001368; TNFR_C6.							
DR Pfam; PF00531; death; 1.							
DR Pfam; PF00020; TNFR_C6; 4.							
DR SMART; SM00208; TNFR; 1.							
DR PROSITE; PS00052; TNFR_NGFR_1; 3.							
DR PROSITE; PS00050; TNFR_NGFR_2; 4.							
KW Receptor; Apoptosis; Neurogenesis; Transmembrane; Glycoprotein;							
KW SIGNAL; Signal.							
FT CHAIN 1 21 BY SIMILARITY.							
FT DOMAIN 22 417 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 16.							
FT TRANSMEM 22 246 EXTRACELLULAR (POTENTIAL).							
FT DOMAIN 247 265 POTENTIAL.							
FT REPEAT 266 417 CYTOPLASMIC (POTENTIAL).							
FT REPEAT 24 57 TNFR_CYS_1.							
FT REPEAT 59 100 TNFR_CYS_2.							
FT REPEAT 101 139 TNFR_CYS_3.							
FT REPEAT 141 181 TNFR_CYS_4.							
FT DOMAIN 346 411 DEATH.							
FT DOMAIN 190 241 SER/THR-RICH.							
FT DISULFID 25 36 BY SIMILARITY.							
Query Match	19 38;	Score 181.5;	DB 1;	Length 41;			
Best Local Similarity	31.5%;	Pred. No. 1.9e-18;					
Matches	51;	Mismatches	25;	Indels	19;	Gaps	10;
QY 4 CPQGKYIHPQNNNSICCTKCHKGTYLYNDCCPGQDIDCRSC-EGGSFTASENHRLRHLCLSC 62							
Db 25 CSTGMTH- -SGECKAKCNGEQAQPC-GANQ-TVCEPCLDSTFSQDSATEPCKPC 79							
QY 63 SKRCKEMQVBEISS-CTVDRDTVCGRKKNQYRHWSNLFCQFCNSLCLNGT-VHLSQE 120							
Db 80 TBC-- -LGLOMSMAPVEADDAVCRVC-- -SYGYQDDEETGRCEACSVGVGSGIVFSCOD 133							
QY 121 KONTYC-TCHAGEFLRE-- -NECVYCSNQKKSLECTKLCP 157							
Db 134 KQNTVCEBCEPEGTYSDEANHVDPCLTVCEDETERQLRECTP 175							
RESULT 12							
TR1B_MOUSE							
ID TR1B_MOUSE							
STANDARD;							
AC P2519; P97893;							
DT 01-MAY-1992 (Rel. 22, Created)							
DT 01-MAY-1992 (Rel. 22, Last sequence update)							
DE Tumor necrosis factor receptor superfamily member 1B precursor (Tumor necrosis factor receptor superfamily receptor 2) (TNF-R2) (p75).							
DE necrosis factor receptor 2 (TNF-R2) (p75).							
OS Mus musculus (Mouse).							
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherea; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
CC NCBI_TaxID=10030;							
RN [1]							
SEQUENCE FROM N.A.							
RX MEDLINE=9118785; PubMed=1849278;							
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.J., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;							
RT Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific.;							
RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834 (1991).							
[2]							
SEQUENCE FROM N.A.							
RX MEDLINE=91246168; PubMed=1645445;							
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;							
RA "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor.";							
RT Mol. Cell. Biol. 11:3020-3026(1991).							
[3]							
SEQUENCE OF 1-26 FROM N.A.							
RP STRAIN=NOD;							
RC Jacob C.O., Liu J.;							
RA Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.							
[4]							
SEQUENCE OF 1-22 FROM N.A.							
RP TISSUE=Liver;							
RC RA Kissane D., Fallowes R., Feldmann M., Chernajovsky Y.;							
RA Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.							
RL CC -!- FUNCTION: Receptor with high affinity for TNFSF2/TNF-alpha and							





CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial/  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----

DR EMBL; AJ00102; CAA04596.1; --.  
 DR HSSP; P25445; IDPF.  
 DR InterPro; IPR00488; Death.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00050; TNFR\_C6; 3.  
 DR SMART; SM0005; DEATH; 1.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE; PS0050; TNFR\_NGFR\_2; 2.  
 DR PROSITE; PS0017; DEATH DOMAIN; 1.  
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 332 TUMOR NECROSIS FACTOR RECEPTOR  
 FT DOMAIN 17 175 SUPERFAMILY MEMBER 6.  
 FT TRANSMEM 176 192 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 45 81 TNFR-CYS 1.  
 FT REPEAT 82 125 TNFR-CYS 2.  
 FT REPEAT 126 164 TNFR-CYS 3.  
 FT DOMAIN 227 311 DEATH.  
 FT DISULFID 46 57 BY SIMILARITY.  
 FT DISULFID 58 71 BY SIMILARITY.  
 FT DISULFID 61 80 BY SIMILARITY.  
 FT DISULFID 83 99 BY SIMILARITY.  
 FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 141 BY SIMILARITY.  
 FT DISULFID 144 155 BY SIMILARITY.  
 FT DISULFID 147 163 BY SIMILARITY.  
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 332 AA; 37292 MW; 5B8B0382756BF1B CRC64;  
 Query Match 18.8%; Score 176.5; DB 1; Length 332;  
 Best Local Similarity 29.1%; Pred. No. 4.1e-08; DB 1;  
 Matches 37; Conservative 18; Mismatches 65; Indels 7; Gaps 4;

Qy 1 DSVQPQKKVHPPQNSICCTKHKGTLYNDCTGGPGQPTDCBCESG-SFTIASENHLRHC 59  
 Qy 43 ESECPPEGH--RBGQFCQCPGPKRKHDCTSPGAQCPVCSEGDDYTDKHHHSKC 99  
 Qy 60 LSCSKRKEMGQVEISCTVDRDTVCGRKNQYRHWMSENLCFPNCSLCLNGTVHUSQ 119  
 Db 100 RRCRVGDGHGLEVKRNCRTQNKCRCKPNFFCH--TSQCBHCNPCTCENGIVIE-NCT 156  
 Qy 120 EKQNFTVC 126  
 Db 157 PTSNIKC 163

Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2002, 14:38:48 ; Search time 31 Seconds  
(without alignments)  
1070.116 Million cell updates/sec

Title: US-09-907-263-2  
Perfect score: 941  
Sequence: 1 DSVCPQGKYIHPQNSICCT.....CSNCRKSLECTKLCLPQIEN 161

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTRMBML\_21:  
 1: sp\_archaea:  
 2: sp\_bacteria:  
 3: sp\_fungi:  
 4: sp\_human:  
 5: sp\_invertebrate:  
 6: sp\_mammal:  
 7: sp\_mhc:  
 8: sp\_organelle:  
 9: sp\_phage:  
 10: sp\_plant:  
 11: sp\_rabbit:  
 12: sp\_virus:  
 13: sp\_vertebrate:  
 14: sp\_unclassified:  
 15: sp\_virus:  
 16: sp\_bacteriopl:  
 17: sp\_archeap:  
 18: sp\_archeap:  
 19: sp\_bacteria:  
 20: sp\_fungi:  
 21: sp\_invertebrate:  
 22: sp\_mammal:  
 23: sp\_mhc:  
 24: sp\_organelle:  
 25: sp\_phage:  
 26: sp\_plant:  
 27: sp\_rabbit:  
 28: sp\_virus:  
 29: sp\_vertebrate:  
 30: sp\_unclassified:  
 31: sp\_virus:  
 32: sp\_bacteriopl:  
 33: sp\_archeap:  
 34: sp\_bacteria:  
 35: sp\_fungi:  
 36: sp\_invertebrate:  
 37: sp\_mammal:  
 38: sp\_mhc:  
 39: sp\_organelle:  
 40: sp\_phage:  
 41: sp\_plant:  
 42: sp\_rabbit:  
 43: sp\_virus:  
 44: sp\_vertebrate:  
 45: sp\_unclassified:  
 46: sp\_bacteriopl:  
 47: sp\_archeap:  
 48: sp\_bacteria:  
 49: sp\_fungi:  
 50: sp\_invertebrate:  
 51: sp\_mammal:  
 52: sp\_mhc:  
 53: sp\_organelle:  
 54: sp\_phage:  
 55: sp\_plant:  
 56: sp\_rabbit:  
 57: sp\_virus:  
 58: sp\_vertebrate:  
 59: sp\_unclassified:  
 60: sp\_bacteriopl:  
 61: sp\_archeap:  
 62: sp\_bacteria:  
 63: sp\_fungi:  
 64: sp\_invertebrate:  
 65: sp\_mammal:  
 66: sp\_mhc:  
 67: sp\_organelle:  
 68: sp\_phage:  
 69: sp\_plant:  
 70: sp\_rabbit:  
 71: sp\_virus:  
 72: sp\_vertebrate:  
 73: sp\_unclassified:  
 74: sp\_bacteriopl:  
 75: sp\_archeap:  
 76: sp\_bacteria:  
 77: sp\_fungi:  
 78: sp\_invertebrate:  
 79: sp\_mammal:  
 80: sp\_mhc:  
 81: sp\_organelle:  
 82: sp\_phage:  
 83: sp\_plant:  
 84: sp\_rabbit:  
 85: sp\_virus:  
 86: sp\_vertebrate:  
 87: sp\_unclassified:  
 88: sp\_bacteriopl:  
 89: sp\_archeap:  
 90: sp\_bacteria:  
 91: sp\_fungi:  
 92: sp\_invertebrate:  
 93: sp\_mammal:  
 94: sp\_mhc:  
 95: sp\_organelle:  
 96: sp\_phage:  
 97: sp\_plant:  
 98: sp\_rabbit:  
 99: sp\_virus:  
 100: sp\_vertebrate:  
 101: sp\_unclassified:  
 102: sp\_bacteriopl:  
 103: sp\_archeap:  
 104: sp\_bacteria:  
 105: sp\_fungi:  
 106: sp\_invertebrate:  
 107: sp\_mammal:  
 108: sp\_mhc:  
 109: sp\_organelle:  
 110: sp\_phage:  
 111: sp\_plant:  
 112: sp\_rabbit:  
 113: sp\_virus:  
 114: sp\_vertebrate:  
 115: sp\_unclassified:  
 116: sp\_bacteriopl:  
 117: sp\_archeap:  
 118: sp\_bacteria:  
 119: sp\_fungi:  
 120: sp\_invertebrate:  
 121: sp\_mammal:  
 122: sp\_mhc:  
 123: sp\_organelle:  
 124: sp\_phage:  
 125: sp\_plant:  
 126: sp\_rabbit:  
 127: sp\_virus:  
 128: sp\_vertebrate:  
 129: sp\_unclassified:  
 130: sp\_bacteriopl:  
 131: sp\_archeap:  
 132: sp\_bacteria:  
 133: sp\_fungi:  
 134: sp\_invertebrate:  
 135: sp\_mammal:  
 136: sp\_mhc:  
 137: sp\_organelle:  
 138: sp\_phage:  
 139: sp\_plant:  
 140: sp\_rabbit:  
 141: sp\_virus:  
 142: sp\_vertebrate:  
 143: sp\_unclassified:  
 144: sp\_bacteriopl:  
 145: sp\_archeap:  
 146: sp\_bacteria:  
 147: sp\_fungi:  
 148: sp\_invertebrate:  
 149: sp\_mammal:  
 150: sp\_mhc:  
 151: sp\_organelle:  
 152: sp\_phage:  
 153: sp\_plant:  
 154: sp\_rabbit:  
 155: sp\_virus:  
 156: sp\_vertebrate:  
 157: sp\_unclassified:  
 158: sp\_bacteriopl:  
 159: sp\_archeap:  
 160: sp\_bacteria:  
 161: sp\_fungi:  
 162: sp\_invertebrate:  
 163: sp\_mammal:  
 164: sp\_mhc:  
 165: sp\_organelle:  
 166: sp\_phage:  
 167: sp\_plant:  
 168: sp\_rabbit:  
 169: sp\_virus:  
 170: sp\_vertebrate:  
 171: sp\_unclassified:  
 172: sp\_bacteriopl:  
 173: sp\_archeap:  
 174: sp\_bacteria:  
 175: sp\_fungi:  
 176: sp\_invertebrate:  
 177: sp\_mammal:  
 178: sp\_mhc:  
 179: sp\_organelle:  
 180: sp\_phage:  
 181: sp\_plant:  
 182: sp\_rabbit:  
 183: sp\_virus:  
 184: sp\_vertebrate:  
 185: sp\_unclassified:  
 186: sp\_bacteriopl:  
 187: sp\_archeap:  
 188: sp\_bacteria:  
 189: sp\_fungi:  
 190: sp\_invertebrate:  
 191: sp\_mammal:  
 192: sp\_mhc:  
 193: sp\_organelle:  
 194: sp\_phage:  
 195: sp\_plant:  
 196: sp\_rabbit:  
 197: sp\_virus:  
 198: sp\_vertebrate:  
 199: sp\_unclassified:  
 200: sp\_bacteriopl:  
 201: sp\_archeap:  
 202: sp\_bacteria:  
 203: sp\_fungi:  
 204: sp\_invertebrate:  
 205: sp\_mammal:  
 206: sp\_mhc:  
 207: sp\_organelle:  
 208: sp\_phage:  
 209: sp\_plant:  
 210: sp\_rabbit:  
 211: sp\_virus:  
 212: sp\_vertebrate:  
 213: sp\_unclassified:  
 214: sp\_bacteriopl:  
 215: sp\_archeap:  
 216: sp\_bacteria:  
 217: sp\_fungi:  
 218: sp\_invertebrate:  
 219: sp\_mammal:  
 220: sp\_mhc:  
 221: sp\_organelle:  
 222: sp\_phage:  
 223: sp\_plant:  
 224: sp\_rabbit:  
 225: sp\_virus:  
 226: sp\_vertebrate:  
 227: sp\_unclassified:  
 228: sp\_bacteriopl:  
 229: sp\_archeap:  
 230: sp\_bacteria:  
 231: sp\_fungi:  
 232: sp\_invertebrate:  
 233: sp\_mammal:  
 234: sp\_mhc:  
 235: sp\_organelle:  
 236: sp\_phage:  
 237: sp\_plant:  
 238: sp\_rabbit:  
 239: sp\_virus:  
 240: sp\_vertebrate:  
 241: sp\_unclassified:  
 242: sp\_bacteriopl:  
 243: sp\_archeap:  
 244: sp\_bacteria:  
 245: sp\_fungi:  
 246: sp\_invertebrate:  
 247: sp\_mammal:  
 248: sp\_mhc:  
 249: sp\_organelle:  
 250: sp\_phage:  
 251: sp\_plant:  
 252: sp\_rabbit:  
 253: sp\_virus:  
 254: sp\_vertebrate:  
 255: sp\_unclassified:  
 256: sp\_bacteriopl:  
 257: sp\_archeap:  
 258: sp\_bacteria:  
 259: sp\_fungi:  
 260: sp\_invertebrate:  
 261: sp\_mammal:  
 262: sp\_mhc:  
 263: sp\_organelle:  
 264: sp\_phage:  
 265: sp\_plant:  
 266: sp\_rabbit:  
 267: sp\_virus:  
 268: sp\_vertebrate:  
 269: sp\_unclassified:  
 270: sp\_bacteriopl:  
 271: sp\_archeap:  
 272: sp\_bacteria:  
 273: sp\_fungi:  
 274: sp\_invertebrate:  
 275: sp\_mammal:  
 276: sp\_mhc:  
 277: sp\_organelle:  
 278: sp\_phage:  
 279: sp\_plant:  
 280: sp\_rabbit:  
 281: sp\_virus:  
 282: sp\_vertebrate:  
 283: sp\_unclassified:  
 284: sp\_bacteriopl:  
 285: sp\_archeap:  
 286: sp\_bacteria:  
 287: sp\_fungi:  
 288: sp\_invertebrate:  
 289: sp\_mammal:  
 290: sp\_mhc:  
 291: sp\_organelle:  
 292: sp\_phage:  
 293: sp\_plant:  
 294: sp\_rabbit:  
 295: sp\_virus:  
 296: sp\_vertebrate:  
 297: sp\_unclassified:  
 298: sp\_bacteriopl:  
 299: sp\_archeap:  
 300: sp\_bacteria:  
 301: sp\_fungi:  
 302: sp\_invertebrate:  
 303: sp\_mammal:  
 304: sp\_mhc:  
 305: sp\_organelle:  
 306: sp\_phage:  
 307: sp\_plant:  
 308: sp\_rabbit:  
 309: sp\_virus:  
 310: sp\_vertebrate:  
 311: sp\_unclassified:  
 312: sp\_bacteriopl:  
 313: sp\_archeap:  
 314: sp\_bacteria:  
 315: sp\_fungi:  
 316: sp\_invertebrate:  
 317: sp\_mammal:  
 318: sp\_mhc:  
 319: sp\_organelle:  
 320: sp\_phage:  
 321: sp\_plant:  
 322: sp\_rabbit:  
 323: sp\_virus:  
 324: sp\_vertebrate:  
 325: sp\_unclassified:  
 326: sp\_bacteriopl:  
 327: sp\_archeap:  
 328: sp\_bacteria:  
 329: sp\_fungi:  
 330: sp\_invertebrate:  
 331: sp\_mammal:  
 332: sp\_mhc:  
 333: sp\_organelle:  
 334: sp\_phage:  
 335: sp\_plant:  
 336: sp\_rabbit:  
 337: sp\_virus:  
 338: sp\_vertebrate:  
 339: sp\_unclassified:  
 340: sp\_bacteriopl:  
 341: sp\_archeap:  
 342: sp\_bacteria:  
 343: sp\_fungi:  
 344: sp\_invertebrate:  
 345: sp\_mammal:  
 346: sp\_mhc:  
 347: sp\_organelle:  
 348: sp\_phage:  
 349: sp\_plant:  
 350: sp\_rabbit:  
 351: sp\_virus:  
 352: sp\_vertebrate:  
 353: sp\_unclassified:  
 354: sp\_bacteriopl:  
 355: sp\_archeap:  
 356: sp\_bacteria:  
 357: sp\_fungi:  
 358: sp\_invertebrate:  
 359: sp\_mammal:  
 360: sp\_mhc:  
 361: sp\_organelle:  
 362: sp\_phage:  
 363: sp\_plant:  
 364: sp\_rabbit:  
 365: sp\_virus:  
 366: sp\_vertebrate:  
 367: sp\_unclassified:  
 368: sp\_bacteriopl:  
 369: sp\_archeap:  
 370: sp\_bacteria:  
 371: sp\_fungi:  
 372: sp\_invertebrate:  
 373: sp\_mammal:  
 374: sp\_mhc:  
 375: sp\_organelle:  
 376: sp\_phage:  
 377: sp\_plant:  
 378: sp\_rabbit:  
 379: sp\_virus:  
 380: sp\_vertebrate:  
 381: sp\_unclassified:  
 382: sp\_bacteriopl:  
 383: sp\_archeap:  
 384: sp\_bacteria:  
 385: sp\_fungi:  
 386: sp\_invertebrate:  
 387: sp\_mammal:  
 388: sp\_mhc:  
 389: sp\_organelle:  
 390: sp\_phage:  
 391: sp\_plant:  
 392: sp\_rabbit:  
 393: sp\_virus:  
 394: sp\_vertebrate:  
 395: sp\_unclassified:  
 396: sp\_bacteriopl:  
 397: sp\_archeap:  
 398: sp\_bacteria:  
 399: sp\_fungi:  
 400: sp\_invertebrate:  
 401: sp\_mammal:  
 402: sp\_mhc:  
 403: sp\_organelle:  
 404: sp\_phage:  
 405: sp\_plant:  
 406: sp\_rabbit:  
 407: sp\_virus:  
 408: sp\_vertebrate:  
 409: sp\_unclassified:  
 410: sp\_bacteriopl:  
 411: sp\_archeap:  
 412: sp\_bacteria:  
 413: sp\_fungi:  
 414: sp\_invertebrate:  
 415: sp\_mammal:  
 416: sp\_mhc:  
 417: sp\_organelle:  
 418: sp\_phage:  
 419: sp\_plant:  
 420: sp\_rabbit:  
 421: sp\_virus:  
 422: sp\_vertebrate:  
 423: sp\_unclassified:  
 424: sp\_bacteriopl:  
 425: sp\_archeap:  
 426: sp\_bacteria:  
 427: sp\_fungi:  
 428: sp\_invertebrate:  
 429: sp\_mammal:  
 430: sp\_mhc:  
 431: sp\_organelle:  
 432: sp\_phage:  
 433: sp\_plant:  
 434: sp\_rabbit:  
 435: sp\_virus:  
 436: sp\_vertebrate:  
 437: sp\_unclassified:  
 438: sp\_bacteriopl:  
 439: sp\_archeap:  
 440: sp\_bacteria:  
 441: sp\_fungi:  
 442: sp\_invertebrate:  
 443: sp\_mammal:  
 444: sp\_mhc:  
 445: sp\_organelle:  
 446: sp\_phage:  
 447: sp\_plant:  
 448: sp\_rabbit:  
 449: sp\_virus:  
 450: sp\_vertebrate:  
 451: sp\_unclassified:  
 452: sp\_bacteriopl:  
 453: sp\_archeap:  
 454: sp\_bacteria:  
 455: sp\_fungi:  
 456: sp\_invertebrate:  
 457: sp\_mammal:  
 458: sp\_mhc:  
 459: sp\_organelle:  
 460: sp\_phage:  
 461: sp\_plant:  
 462: sp\_rabbit:  
 463: sp\_virus:  
 464: sp\_vertebrate:  
 465: sp\_unclassified:  
 466: sp\_bacteriopl:  
 467: sp\_archeap:  
 468: sp\_bacteria:  
 469: sp\_fungi:  
 470: sp\_invertebrate:  
 471: sp\_mammal:  
 472: sp\_mhc:  
 473: sp\_organelle:  
 474: sp\_phage:  
 475: sp\_plant:  
 476: sp\_rabbit:  
 477: sp\_virus:  
 478: sp\_vertebrate:  
 479: sp\_unclassified:  
 480: sp\_bacteriopl:  
 481: sp\_archeap:  
 482: sp\_bacteria:  
 483: sp\_fungi:  
 484: sp\_invertebrate:  
 485: sp\_mammal:  
 486: sp\_mhc:  
 487: sp\_organelle:  
 488: sp\_phage:  
 489: sp\_plant:  
 490: sp\_rabbit:  
 491: sp\_virus:  
 492: sp\_vertebrate:  
 493: sp\_unclassified:  
 494: sp\_bacteriopl:  
 495: sp\_archeap:  
 496: sp\_bacteria:  
 497: sp\_fungi:  
 498: sp\_invertebrate:  
 499: sp\_mammal:  
 500: sp\_mhc:  
 501: sp\_organelle:  
 502: sp\_phage:  
 503: sp\_plant:  
 504: sp\_rabbit:  
 505: sp\_virus:  
 506: sp\_vertebrate:  
 507: sp\_unclassified:  
 508: sp\_bacteriopl:  
 509: sp\_archeap:  
 510: sp\_bacteria:  
 511: sp\_fungi:  
 512: sp\_invertebrate:  
 513: sp\_mammal:  
 514: sp\_mhc:  
 515: sp\_organelle:  
 516: sp\_phage:  
 517: sp\_plant:  
 518: sp\_rabbit:  
 519: sp\_virus:  
 520: sp\_vertebrate:  
 521: sp\_unclassified:  
 522: sp\_bacteriopl:  
 523: sp\_archeap:  
 524: sp\_bacteria:  
 525: sp\_fungi:  
 526: sp\_invertebrate:  
 527: sp\_mammal:  
 528: sp\_mhc:  
 529: sp\_organelle:  
 530: sp\_phage:  
 531: sp\_plant:  
 532: sp\_rabbit:  
 533: sp\_virus:  
 534: sp\_vertebrate:  
 535: sp\_unclassified:  
 536: sp\_bacteriopl:  
 537: sp\_archeap:  
 538: sp\_bacteria:  
 539: sp\_fungi:  
 540: sp\_invertebrate:  
 541: sp\_mammal:  
 542: sp\_mhc:  
 543: sp\_organelle:  
 544: sp\_phage:  
 545: sp\_plant:  
 546: sp\_rabbit:  
 547: sp\_virus:  
 548: sp\_vertebrate:  
 549: sp\_unclassified:  
 550: sp\_bacteriopl:  
 551: sp\_archeap:  
 552: sp\_bacteria:  
 553: sp\_fungi:  
 554: sp\_invertebrate:  
 555: sp\_mammal:  
 556: sp\_mhc:  
 557: sp\_organelle:  
 558: sp\_phage:  
 559: sp\_plant:  
 560: sp\_rabbit:  
 561: sp\_virus:  
 562: sp\_vertebrate:  
 563: sp\_unclassified:  
 564: sp\_bacteriopl:  
 565: sp\_archeap:  
 566: sp\_bacteria:  
 567: sp\_fungi:  
 568: sp\_invertebrate:  
 569: sp\_mammal:  
 570: sp\_mhc:  
 571: sp\_organelle:  
 572: sp\_phage:  
 573: sp\_plant:  
 574: sp\_rabbit:  
 575: sp\_virus:  
 576: sp\_vertebrate:  
 577: sp\_unclassified:  
 578: sp\_bacteriopl:  
 579: sp\_archeap:  
 580: sp\_bacteria:  
 581: sp\_fungi:  
 582: sp\_invertebrate:  
 583: sp\_mammal:  
 584: sp\_mhc:  
 585: sp\_organelle:  
 586: sp\_phage:  
 587: sp\_plant:  
 588: sp\_rabbit:  
 589: sp\_virus:  
 590: sp\_vertebrate:  
 591: sp\_unclassified:  
 592: sp\_bacteriopl:  
 593: sp\_archeap:  
 594: sp\_bacteria:  
 595: sp\_fungi:  
 596: sp\_invertebrate:  
 597: sp\_mammal:  
 598: sp\_mhc:  
 599: sp\_organelle:  
 600: sp\_phage:  
 601: sp\_plant:  
 602: sp\_rabbit:  
 603: sp\_virus:  
 604: sp\_vertebrate:  
 605: sp\_unclassified:  
 606: sp\_bacteriopl:  
 607: sp\_archeap:  
 608: sp\_bacteria:  
 609: sp\_fungi:  
 610: sp\_invertebrate:  
 611: sp\_mammal:  
 612: sp\_mhc:  
 613: sp\_organelle:  
 614: sp\_phage:  
 615: sp\_plant:  
 616: sp\_rabbit:  
 617: sp\_virus:  
 618: sp\_vertebrate:  
 619: sp\_unclassified:  
 620: sp\_bacteriopl:  
 621: sp\_archeap:  
 622: sp\_bacteria:  
 623: sp\_fungi:  
 624: sp\_invertebrate:  
 625: sp\_mammal:  
 626: sp\_mhc:  
 627: sp\_organelle:  
 628: sp\_phage:  
 629: sp\_plant:  
 630: sp\_rabbit:  
 631: sp\_virus:  
 632: sp\_vertebrate:  
 633: sp\_unclassified:  
 634: sp\_bacteriopl:  
 635: sp\_archeap:  
 636: sp\_bacteria:  
 637: sp\_fungi:  
 638: sp\_invertebrate:  
 639: sp\_mammal:  
 640: sp\_mhc:  
 641: sp\_organelle:  
 642: sp\_phage:  
 643: sp\_plant:  
 644: sp\_rabbit:  
 645: sp\_virus:  
 646: sp\_vertebrate:  
 647: sp\_unclassified:  
 648: sp\_bacteriopl:  
 649: sp\_archeap:  
 650: sp\_bacteria:  
 651: sp\_fungi:  
 652: sp\_invertebrate:  
 653: sp\_mammal:  
 654: sp\_mhc:  
 655: sp\_organelle:  
 656: sp\_phage:  
 657: sp\_plant:  
 658: sp\_rabbit:  
 659: sp\_virus:  
 660: sp\_vertebrate:  
 661: sp\_unclassified:  
 662: sp\_bacteriopl:  
 663: sp\_archeap:  
 664: sp\_bacteria:  
 665: sp\_fungi:  
 666: sp\_invertebrate:  
 667: sp\_mammal:  
 668: sp\_mhc:  
 669: sp\_organelle:  
 670: sp\_phage:  
 671: sp\_plant:  
 672: sp\_rabbit:  
 673: sp\_virus:  
 674: sp\_vertebrate:  
 675: sp\_unclassified:  
 676: sp\_bacteriopl:  
 677: sp\_archeap:  
 678: sp\_bacteria:  
 679: sp\_fungi:  
 680: sp\_invertebrate:  
 681: sp\_mammal:  
 682: sp\_mhc:  
 683: sp\_organelle:  
 684: sp\_phage:  
 685: sp\_plant:  
 686: sp\_rabbit:  
 687: sp\_virus:  
 688: sp\_vertebrate:  
 689: sp\_unclassified:  
 690: sp\_bacteriopl:  
 691: sp\_archeap:  
 692: sp\_bacteria:  
 693: sp\_fungi:  
 694: sp\_invertebrate:  
 695: sp\_mammal:  
 696: sp\_mhc:  
 697: sp\_organelle:  
 698: sp\_phage:  
 699: sp\_plant:  
 700: sp\_rabbit:  
 701: sp\_virus:  
 702: sp\_vertebrate:  
 703: sp\_unclassified:  
 704: sp\_bacteriopl:  
 705: sp\_archeap:  
 706: sp\_bacteria:  
 707: sp\_fungi:  
 708: sp\_invertebrate:  
 709: sp\_mammal:  
 710: sp\_mhc:  
 711: sp\_organelle:  
 712: sp\_phage:  
 713: sp\_plant:  
 714: sp\_rabbit:  
 715: sp\_virus:  
 716: sp\_vertebrate:  
 717: sp\_unclassified:  
 718: sp\_bacteriopl:  
 719: sp\_archeap:  
 720: sp\_bacteria:  
 721: sp\_fungi:  
 722: sp\_invertebrate:  
 723: sp\_mammal:  
 724: sp\_mhc:  
 725: sp\_organelle:  
 726: sp\_phage:  
 727: sp\_plant:  
 728: sp\_rabbit:  
 729: sp\_virus:  
 730: sp\_vertebrate:  
 731: sp\_unclassified:  
 732: sp\_bacteriopl:  
 733: sp\_archeap:  
 734: sp\_bacteria:  
 735: sp\_fungi:  
 736: sp\_invertebrate:  
 737: sp\_mammal:  
 738: sp\_mhc:  
 739: sp\_organelle:  
 740: sp\_phage:  
 741: sp\_plant:  
 742: sp\_rabbit:  
 743: sp\_virus:  
 744: sp\_vertebrate:  
 745: sp\_unclassified:  
 746: sp\_bacteriopl:  
 747: sp\_archeap:  
 748: sp\_bacteria:  
 749: sp\_fungi:  
 750: sp\_invertebrate:  
 751: sp\_mammal:  
 752: sp\_mhc:  
 753: sp\_organelle:  
 754: sp\_phage:  
 755: sp\_plant:  
 756: sp\_rabbit:  
 757: sp\_virus:  
 758: sp\_vertebrate:  
 759: sp\_unclassified:  
 760: sp\_bacteriopl:  
 761: sp\_archeap:  
 762: sp\_bacteria:  
 763: sp\_fungi:  
 764: sp\_invertebrate:  
 765: sp\_mammal:  
 766: sp\_mhc:  
 767: sp\_organelle:  
 768: sp\_phage:  
 769: sp\_plant:  
 770: sp\_rabbit:  
 771: sp\_virus:  
 772: sp\_vertebrate:  
 773: sp\_unclassified:  
 774: sp\_bacteriopl:  
 775: sp\_archeap:  
 776: sp\_bacteria:  
 777: sp\_fungi:  
 778: sp\_invertebrate:  
 779: sp\_mammal:  
 780: sp\_mhc:  
 781: sp\_organelle:  
 782: sp\_phage:  
 783: sp\_plant:  
 784: sp\_rabbit:  
 785: sp\_virus:  
 786: sp\_vertebrate:  
 787: sp\_unclassified:  
 788: sp\_bacteriopl:  
 789: sp\_archeap:  
 790: sp\_bacteria:  
 791: sp\_fungi:  
 792: sp\_invertebrate:  
 793: sp\_mammal:  
 794: sp\_mhc:  
 795: sp\_organelle:  
 796: sp\_phage:  
 797: sp\_plant:  
 798: sp\_rabbit:  
 799: sp\_virus:  
 800: sp\_vertebrate:  
 801: sp\_unclassified:  
 802: sp\_bacteriopl:  
 803: sp\_archeap:  
 804: sp\_bacteria:  
 805: sp\_fungi:  
 806: sp\_invertebrate:  
 807: sp\_mammal:  
 808: sp\_mhc:  
 809: sp\_organelle:  
 810: sp\_phage:  
 811: sp\_plant:  
 812: sp\_rabbit:  
 813: sp\_virus:  
 814: sp\_vertebrate:  
 815: sp\_unclassified:  
 816: sp\_bacteriopl:  
 817: sp\_archeap:  
 818: sp\_bacteria:  
 819: sp\_fungi:  
 820: sp\_invertebrate:  
 821: sp\_mammal:  
 822: sp\_mhc:  
 823: sp\_organelle:  
 824: sp\_phage:  
 825: sp\_plant:  
 826: sp\_rabbit:  
 827: sp\_virus:  
 828: sp\_vertebrate:  
 829: sp\_unclassified:  
 830: sp\_bacteriopl:  
 831: sp\_archeap:  
 832: sp\_bacteria:  
 833: sp\_fungi:  
 834: sp\_invertebrate:  
 835: sp\_mammal:  
 836: sp\_mhc:  
 837: sp\_organelle:  
 838: sp\_phage:  
 839: sp\_plant:  
 840: sp\_rabbit:  
 841: sp\_virus:  
 842: sp\_vertebrate:  
 843: sp\_unclassified:  
 844: sp\_bacteriopl:  
 845: sp\_archeap:  
 846: sp\_bacteria:  
 847: sp\_fungi:  
 848: sp\_invertebrate:  
 849: sp\_mammal:  
 850: sp\_mhc:  
 851: sp\_organelle:  
 852: sp\_phage:  
 853: sp\_plant:  
 854: sp\_rabbit:  
 855: sp\_virus:  
 856: sp\_vertebrate:  
 857: sp\_unclassified:  
 858: sp\_bacteriopl:  
 859: sp\_archeap:  
 860: sp\_bacteria:  
 861: sp\_fungi:  
 862: sp\_invertebrate:  
 863: sp\_mammal:  
 864: sp\_mhc:  
 865: sp\_organelle:  
 866: sp\_phage:  
 867: sp\_plant:  
 868: sp\_rabbit:  
 869: sp\_virus:  
 870: sp\_vertebrate:  
 871: sp\_unclassified:  
 872: sp\_bacteriopl:  
 873: sp\_archeap:  
 874: sp\_bacteria:  
 875: sp\_fungi:  
 876: sp\_invertebrate:  
 877: sp\_mammal:  
 878: sp\_mhc:  
 879: sp\_organelle:  
 880: sp\_phage:  
 881: sp\_plant:  
 882: sp\_rabbit:  
 883: sp\_virus:  
 884: sp\_vertebrate

OY	4	CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS	63	OC
Db	44	CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS	103	OC Mammalia; Buteraria; Carnivora; Fissipedia; Felidae; Felis.
OY	64	KCKEMQVEISSTVDRTVCCRKKNQRHYSNLFQCFNSCLINGTVLSCQKQN	123	OX
Db	104	KCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN	163	RN SEQUENCE FROM N.A. Duthie S., Nasir L., Eckersall P.D.; "Felis catus" tumour necrosis factor receptor p60 (TNFR-1) mRNA, partial cds.;" submitted (JAN-1998) to the EMBL/GenBank/DDJB databases.
QY	124	TVTCHAGFFLRENECVCSNCKSLECTKLCIPOIE	160	RT submitted (JAN-1998) to the EMBL/GenBank/DDJB databases.
Db	164	TVTCHAGFFLRENECVCSNCKNTECTKLCPIVE	200	DR EMBL; U72344; AAB95099.1; -.
RESULT 2				DR HSSP; P19438; ITEXT.
ID	097530	PRELIMINARY;	PRT; 189 AA.	DR InterPro; IPRO00561; EGF-like.
AC	097530;			DR InterPro; IPRO01368; TNFR_c6.
DT	01-MAY-1999	(TREMBrel. 10, Created)		DR pfam; PF00020; TNFR_c6; 3.
DT	01-MAY-1999	(TREMBrel. 10, Last sequence update)		DR SMART; SM00208; TNFR_c6; 3.
DE	01-JUN-2002	(TREMBrel. 21, Last annotation update)		DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
OS		Tumor necrosis factor receptor p60 (Fragment).		DR PROSITE; PS00652; TNFR_NGFR_1; 3.
OC		Cannis familiaris (Dog).		DR PROSITE; PS50050; TNFR_NGFR_2; 3.
OC		Mammalia; Buteraria; Carnivora; Fissipedia; Canidae; Canis.		KW Receptor.
OX		NCBI_TaxID:9615;		FT NON_TER 189 189
RN		[1]		SQ SEQUENCE 189 AA; 21420 MW; F3FB0CE809D7DBE CRC64;
RP		SEQUENCE FROM N.A.		Query Match 77.7%; Score 731; DB 6; Length 189;
RC		TISSUE=BRAIN;		Best Local Similarity 85.5%; Pred. No. 1 8e-73; Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0
RX		MEDLINE:21109092; PubMed=11182158;		GT Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0
RA		Campbell S.E., Nasir L., Argyle D.J., Gault E.A., Duthie S.,		QY 4 CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS 63
RA		Bennett D.,		Db 44 CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS 103
RA		"Cloning of canine IL-1 $\alpha$ , TNFR and TNF-2.";		QY 64 KCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN 123
RL		Vet. Immunol. Immunopathol. 78:207-214(2001).		Db 104 KCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN 163
DR		HSSP; P19438; 1TNR.		QY 124 TVTCHAGFFLRENECVCSNCKS 148
DR		InterPro; IPRO00561; EGF-like.		Db 164 TVTCHAGFFLRENECVCSNCKN 188
DR		InterPro; IPRO01368; TNFR_c6.		
DR		Pfam; PF00020; TNFR_c6; 3.		
DR		SMART; SM00208; TNFR_c6; 3.		
DR		PROSITE; PS01186; EGF_2; UNKNOWN_1.		
DR		PROSITE; PS00652; TNFR_NGFR_1; 3.		
DR		PROSITE; PS50050; TNFR_NGFR_2; 3.		
DR		KW Receptor.		
FT		NON_TER 189 189		
SQ		SEQUENCE 189 AA; 21420 MW; F3FB0CE809D7DBE CRC64;		
Query Match 77.7%; Score 731; DB 6; Length 189;				
Best Local Similarity 85.5%; Pred. No. 1 8e-73; Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0				
GT Matches 124; Conservative 8; Mismatches 13; Indels 0; Gaps 0				
QY	4	CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS	63	OC
Db	44	CPOGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSCS	103	OC Mammalia; Buteraria; Carnivora; Fissipedia; Felidae; Felis.
QY	64	KCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN	123	OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Db	104	KCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN	163	OX NCBI_TaxID:10090;
QY	124	TVTCHAGFFLRENECVCSNCKS	148	RN SEQUENCE FROM N.A.
Db	164	TVTCHAGFFLRENECVCSNCKN	188	RC STRAIN=129/SV;
QY	3	VCPGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSC	62	RX MEDLINE:2115384; PubMed=11261933;
Db	43	LCPQGKYHPPONNSICCTKCHKGTYLYNDCAAGPGLDTCRECENGTFASENHLRQLSC	102	RA Wang E.C.Y., Kitson J., Thern A., Williamson J., Farrow S.N.,
QY	63	SKCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN	122	RA Owen M.J.,
Db	103	SKCKEMQVEISPTVYDTCRKNQRHYSNLFQCFNSCLINGTVLSCQKQN	162	RT "Genomic structure, expression, and chromosome mapping of the mouse
QY	123	NTVTCAGFFLRENECVCSNCKS	148	RT homologue for the WSL-1 (DR3, Apo3, TRAMP, LARD, TR3, TNFRSF12)
Db	163	NTVTCAGFFLRENECVCSNCKN	188	RT gene.";
RESULT 3				RL immunogenetics 53:59-63(2001).
ID	095185	PRELIMINARY;	PRT; 189 AA.	DR EMBL; AR229965; AAC11256.1; -.
AC	095185;			DR HSSP; P55942; ICDF.
AC	095185;	(TREMBrel. 02, Created)		DR MGD; MGI:1934667; Tnfrsf12.
DT	01-FEB-1997	(TREMBrel. 02, Last sequence update)		DR InterPro; IPRO00488; Death.
DT	01-JUN-1998	(TREMBrel. 06, Last annotation update)		DR InterPro; IPRO00561; EGF-like.
DT	01-JUN-2002	(TREMBrel. 21, Last annotation update)		DR InterPro; IPRO01368; TNFR_c6.
DE		Tumour necrosis factor receptor p60 (Fragment).		DR pfam; PF00531; death; 1.
OS		Felis silvestris catus (Cat).		DR SMART; SM00208; TNFR_c6; 3.
PROSITE; PS50017; DEATH_DOMAIN; 1.				DR PROSITE; PS50017; DEATH_DOMAIN; 1.

DR PROSITE; PS01186; EGF 2; UNKNOWN\_1.  
 DR PROSITE; PS00652; TNFR\_NGR\_1; UNKNOWN\_1.  
 DR PROSITE; PS5050; TNFR\_NGR\_2; 1.  
 SQ SEQUENCE 413 AA; 44453 MW; 69F21B85D0DABBF CRC64;

Query Match Score 202; DB 11; Length 413;  
 Best Local Similarity 31.4%; Pred. No. 2.3e-14;  
 Matches 48; Conservative 19; Mismatches 58; Indels 28; Gaps 7;

Qy 18 CCTCKRGTLYNDCGPGQDTCCECSFTASENHIR-HCULCSKSKRKENGQVEISSL 76  
 Db 54 CCRGCPKGHNMKAPECPGNSTCPCSDTFLTDNHFRTDCTRCVQCDDEALQVTLEN 11.3  
 Qy 77 CTVDRLTVCGCRKNQYRHYNSENLQCFENSLCLNG-TYHLSC-----QBKONTVCT 12.7  
 Db 114 CSAKSDTHCGQSG-----W-----CVDESTVPGKSSPFSCVPCGATTPVHEAPTPRP 16.2  
 Qy 128 CHAGFFLRENCOVSC----SNCKKSLETCIYL 155  
 Db 163 CLPFGFYTRGNDCTSPTGFSSVCPKA--CTAVC 19.3

RESULT 5  
 Q9PVDA PRELIMINARY; PRT; 387 AA.  
 ID Q9PVDA ; PRELIMINARY; PRT; 387 AA.  
 AC DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)  
 OS DB-like transmembrane protein fullback.  
 OC Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopidae; Xenopidae; Xenopus.  
 RN [1] -  
 RP SEQUENCE FROM N.A.  
 RA Hick E., Sun B.I., Collins-Racie L., LaVallie E., Sive H.L.;  
 RT "Identification and Characterization of fullback, a Novel Posteriorly-  
 Expressed Xenopus Gene.",  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR AF11890; AD54072.1; -.  
 DR HSSP; P0174; INGR.  
 DR InterPro; IPR001083; Copper-fist.  
 DR InterPro; IPR000488; Death.  
 DR Pfam; PF00531; death; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR SMART; SM000412; CU\_FIST; 1.  
 DR SMART; SM00005; DEATH; 1.  
 DR SMART; SM00208; TNFR; 4.  
 DR PROSITE; PS00017; DEATH\_DOMAIN; 1.  
 DR PROSITE; PS00652; TNFR\_NGR\_1; UNKNOWN\_3.  
 KW TRANSMEMBRANE; PS5050; TNFR\_NGR\_2; 4.

SQ SEQUENCE 387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;

Query Match Score 20.5%; DB 13; Length 387;  
 Best Local Similarity 31.9%; Pred. No. 2.2e-13;  
 Matches 53; Conservative 24; Mismatches 71; Indels 18; Gaps 10;

RESULT 6  
 Q91ZM6 PRELIMINARY; PRT; 433 AA.  
 ID Q91ZM6 ; PRELIMINARY; PRT; 433 AA.  
 AC DT 01-DEC-2001 (T-EMBLrel. 19, Created)  
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)  
 DE Tumor necrosis factor receptor type II (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Muridae; Murinae; Sciurognathi; Rodentia; Sciurognathi; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1] -  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-SPRAGUE-DAWLEY;  
 RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;  
 RT TNF-receptors P60 and P80 are constitutively expressed by rat brain capillary endothelial cells and participate in TNF-alpha transport through the blood-brain barrier.;  
 RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AF420214; AAL1021.1; -.  
 DR DR InterPro; IPR01368; TNFR\_c6; -.  
 DR Pfam; PF00020; TNFR\_c6; 4.  
 DR PROSITE; PS000652; TNFR\_NGR\_1; UNKNOWN\_2.  
 DR PROSITE; PS5050; TNFR\_NGR\_2; 3.  
 KW Receptor.

FT NON\_TER 1 1  
 FT NON\_TER 433 433 MW; 75716D835E72CA4A CRC64;  
 SQ SEQUENCE 433 AA; 45723 MW; 75716D835E72CA4A CRC64;

Query Match Score 20.3%; DB 11; Length 433;  
 Best Local Similarity 32.7%; Pred. No. 4e-13;  
 Matches 52; Conservative 18; Mismatches 79; Indels 10; Gaps 7;

Qy 4 CPGKTYTHPQNSICCTKCHRGTYLYNDCGPGQDTCRECESGSFTASENHLRHCLSC- 62  
 Db 20 CQISQEYYDKAQMQCCAKCPGQYAKHFC-NKTSDDTVCADCAAGMFQWVNLHCLSCS 78  
 Qy 63 SKCRKEMGQBEISSCTVDRDTVGCRKKNQY- RHYWSNEIFQOCNCNSLCLNG-TYHLSCQ 11.9  
 Db 79 SSCSDD-QVTHNCTKKQRVCAQNADSYCALKLHSGNRQCMKLSSKGPGFVASRT 13.6  
 Qy 120 EKQNTCT-CHAGFFLRENCEVCSCNCNSLCTKLLP 15.7  
 Db 137 SNGNVTCASACAPGTF--SDTTSSSTDVCRPHRICSTLAIP 17.3

RESULT 7  
 Q9PUS0 PRELIMINARY; PRT; 302 AA.  
 ID Q9PUS0 ; PRELIMINARY; PRT; 302 AA.  
 AC Q9PUS0 ; PRELIMINARY; PRT; 302 AA.  
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)  
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)  
 DE Decoy TNF receptor.  
 OS Salvelinus fontinalis (Brook trout) (Brook char).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.  
 NCBI\_TaxID=8038;

RN [1] -  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2011001; PubMed=10642582;  
 RA Bobe J., Goetz P.W.;  
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in the brook trout (Salvelinus fontinalis) ovary at the completion of ovulation.";  
 DR HSSP; AF116738; AAD56428.1; -.  
 DR HSSP; O14163; 1D4V.  
 DR InterPro; IPR000561; EGFR like.  
 DR InterPro; IPR01368; TNFR\_c6.

Qy 1 DSVCPCGKYTHPQNSICCTKCHRGTYLYNDCGPGQDTCRECESGSFTASENHLRH 59  
 Db 22 EDVCEBSGLY -TNSGKCCSLCPAGFGVVPY-GDSDTIKCECIENSTFSVRSARKC 76  
 Qy 60 LSCKSCKREMGMQBEISSCTVDRDTVGCRKKNQYRHYWSNEIFQOCNCNSLCLNG-TYHLSC 11.8  
 Db 77 QPCFTCQSPSLTE SNCNTQDVTCRERQLD-SNGI -CLPCQLCSKHGIVVSQC 13.1  
 Qy 119 QEKONTVC-TCHAGFFLRL---ENECVSS-SNKWKSLECTKLQLPQ 15.8  
 Db 132 THKNTVQCQCLSSGYSEVKSSESPCLPERTEKETEVOIGDCVCPQ 17.7

DR	Pfam; PF00020; TNFR_c6; 4.
SMART	SM00208; TNFR; 4.
PROSITE	PS01166; EGF_2; UNKNOWN_1.
DR	DR
PROSITE	PS00620; TNFR_NGFR_1; UNKNOWN_1.
DR	DR
KW	Receptor.
SQ	302 AA; 34037 MW; B44C73477F05C3DF CRC64;
Query Match	20.9%; Score 188; DB 13; Length 302;
Best Local Similarity	31.5%; Pred. No. 6.1e-13;
Matches	45; Conservative 21; Mismatches 53; Indels 24; Gaps 7;
Db	33 SIVCDRCPGPGYLRAPCSAM-RKSICACFGKNCVHLSQKRCMNGVQEV 89
Qy	16 SICCTKCHK3JYLYNDCPGPQDQTGRCBESGSFTASENHILRHCLSCSKRKEMQVEIS 75
Db	90 ECSPSNCECTCKEG--YFNKKYBACKKEKCPGPGYGAANTGPH---QPTECQ 140
Qy	128 CHAGFFLRENE---CVSCSNCK 146
Db	141 COAGFSEVSSAKATCLAQSNCK 163
RESULT 8	
ID	Q9DGH7 PRELIMINARY; PRT; 285 AA.
AC	Q9DGH7; 1.
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	Fas ligand receptor soluble form (Fragment).
OS	Gallus gallus (Chicken).
OC	Archosauria; Aves; Neognathae; Chordata; Craniata; Vertebrata; Euteleostomi; Gallus.
OX	NCBI_TaxID=9031;
RN	SEQUENCE FROM N.A.
RP	Bridgman J.T., Johnson A.L.; Expression and Regulation in Hen Granulosa Cells.";
RA	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RT	Fast Expression and Regulation in Hen Granulosa Cells."
RL	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DR	EMLBL; AF296875; AAC02243.1; -.
DR	HSSP; 014763; 1pAV.
DR	InterPro; IPR000488; Death.
DR	InterPro; IPR001368; TNFR_c6.
DR	PFam; PF00531; death; 1.
DR	PFam; PF00020; TNFR_c2.
DR	SMART; SM0008; TNFR; 3.
DR	PROSITE; PS50017; DEATH DOMAIN; 1.
DR	PROSITE; PS50050; TNFR_NGFR_1; UNKNOWN_2.
KW	Receptor.
SQ	357 AA; 46662 MW; 1652B4840D9EEDBA CRC64;
Query Match	19.1%; Score 179.5; DB 13; Length 357;
Best Local Similarity	28.8%; Pred. No. 6.3e-12;
Matches	45; Conservative 15; Mismatches 53; Indels 43; Gaps 3;
Db	38 DVSGRELEYPH---ENICCLNPAGTYVKKACAAARKGVACPCEDTYEHGILKC 94
Qy	1 DSVCPQG-KYTHRONNISTCCTKCHKGTYLYNDCPGPQDQTGRCBESGSFTASENHILRHCLSCSKRKEMQVEIS 59
Db	95 ISCDKCR-IQDTEIEKCSTONTRCKCR-----NCSFCL----- 127
Qy	120 EKQNTVTCAGFFLRENECVCSNCKSLETCILC 155
Db	128 --PDQAC-----EVCKKCSRCKDEETEKSC 151
RESULT 10	
ID	Q57079 PRELIMINARY; PRT; 320 AA.
AC	Q57079; 1.
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-JUN-1998 (TREMBLrel. 06, Last annotation update)
DE	Tumor necrosis factor receptor II homolog (V211).
GN	CRMD.
RN	SEQUENCE FROM N.A.
OS	Cowpox virus (CPV).
OC	Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC	Orthopoxvirus.
NCBI_TaxID=10243;	
RN	[1]_
RP	STRAIN=BRIGHTON;
RX	MEDLINE=98116382; PubMed=952045;
6	CCTKCKKRHKVKSIDCPKTOE-HCVPCKGEYMDHINDLDCMRCSRSDKAIGLEVKN 63
Qy	77 CTYDRDTVGCGKRNQHYWSENLFQFCNSCLNGVHLSQEKONTVC 126
Db	64 CTSTENAECCSAKNHYCN--SSRCHECSTVCENGSOIEKETSTSSTDTCV 111
RESULT 9	
RX	MEDLINE=83117629; PubMed=6961398;



RL	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.	Db	133 -KCDSSGVVGYSSKGVDVCKKCPGNID 159
DR	EMBL; AF96874; AGO2242; 1; .	RESULT 14	
DR	HSSP; O14763; ID4V.	ID	057092 PRELIMINARY; PRT; 316 AA.
DR	InterPro; IPR00488; Death.	DR	057092; SMART; SM0005; DEATH; 1.
DR	InterPro; IPR001368; TNFR_c6.	DR	SMART; SM0028; TNFR; 2.
DR	Pfam; PF00531; death; 1.	DR	PROSITE; PS0052; TNFR_NGFR_1; UNKNOWN_1.
DR	Pfam; PF00020; TNFR_c6; 2.	DR	PROSITE; PS0052; TNFR_NGFR_2; 2.
FT	NON_TER; 1	SQ	SEQUENCE 312 AA; 35275 MW; 5496BCF1E4CB676C CRC64;
Query Match	18.7%; Score 175.5; DB 13; length 312; Matches 36; Conservative 32.7%; pred. No. 1.6e-11; Mismatches 55; Indels 5; Gaps 3; OS	Qy	18 CCTKKCHKGTYLYNQCPGPQGDTCRCESG-SFWASENHLRHLSCKRKENGQVLISS 76
Matches	36; Conservative 32.7%; pred. No. 1.6e-11; Mismatches 55; Indels 5; Gaps 3; OS	Db	6 CCTTKCRGHVKSTID--PKTQAHCPVRKSGEYMDHINDLDECWRCRCSDKAIGLEVVKN 63
Qy	77 CTIVRDIVCGCRKNQYRHSENIFQCFNCSLCLNGTVHLSCBQKQNTVC 126	Qy	77 CTIVRDIVCGCRKNQYRHSENIFQCFNCSLCLNGTVHLSCBQKQNTVC 126
Db	64 CTSTENAECSCAKHYN--SSRCBHCESCTVCENGQIEKECTSPTVC 111	Db	64 CTSTENAECSCAKHYN--SSRCBHCESCTVCENGQIEKECTSPTVC 111
RESULT 13		RESULT 13	
ID	072761 PRELIMINARY; PRT; 322 AA.	ID	072761 PRELIMINARY; PRT; 322 AA.
AC	072761; SMART; SM00208; TNFR_c6; 2.	AC	072761; SMART; SM00208; TNFR_c6; 2.
DT	01-AUG-1998 (REMBrel. 07, Last sequence update)	DT	01-AUG-1998 (REMBrel. 07, Last sequence update)
DT	01-JUN-2002 (REMBrel. 21, Last annotation update)	DT	01-JUN-2002 (REMBrel. 21, Last annotation update)
DE	K2R protein.	DE	K2R protein.
GN	Cowpox virus (CPV).	GN	Cowpox virus (CPV).
OS	Viruses; dsDNA viruses; Orthopoxvirus.	OS	Viruses; dsDNA viruses; Orthopoxvirus.
OC	NCBI_TaxID=10243; RN [1]	OC	NCBI_TaxID=10243; RN [1]
OX	SEQUENCE FROM N.A.	OX	SEQUENCE FROM N.A.
RP	SETRAMELLIA virus.	RP	SETRAMELLIA virus.
RC	REceptor.	RC	REceptor.
RX	MEDLINE=9818822; PubMed=9520445;	RX	MEDLINE=9818822; PubMed=9520445;
RA	Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,	RA	Buller R.M.L., Pickup D.J., Espiritu J.J.;
RA	"A third distinct tumor necrosis factor receptor of orthopoxviruses.";	RA	"A third distinct tumor necrosis factor receptor of orthopoxviruses.";
RT	PROC. NATL. ACAD. SCI. U.S.A. 95:3786-3791(1998).	RT	PROC. NATL. ACAD. SCI. U.S.A. 95:3786-3791(1998).
RL	EMBL; U87578; AAC93501; 1; .	RL	EMBL; U87578; AAC93501; 1; .
DR	InterPro; IPR001368; TNFR_c6.	DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 2.	DR	Pfam; PF00020; TNFR_c6; 2.
DR	PROSITE; PS0052; TNFR_NGFR_1; 2.	DR	PROSITE; PS0052; TNFR_NGFR_2; 2.
DR	PROSITE; PS0052; TNFR_NGFR_2; 2.	DR	PROSITE; PS0052; TNFR_NGFR_2; 2.
KW	RECEPTOR	KW	RECEPTOR
SQ	SEQUENCE 316 AA; 34660 MW; 443CC1185B4E12A9 CRC64;	SQ	SEQUENCE 316 AA; 34660 MW; 443CC1185B4E12A9 CRC64;
Query Match	18.2%; Score 171.5; DB 12; Length 316; Matches 42; Conservative 27.8%; Pred. No. 4.4e-11; Mismatches 22; Indels 25; Gaps 6; OS	Qy	14 NNSICCTKCHKGTYLYNQCPGPQGDTCRCESGSFASSENHLRHLSCKRKENGQV 72
Best Local Similarity	18.2%; Score 171.5; DB 12; Length 316; Matches 42; Conservative 27.8%; Pred. No. 4.4e-11; Mismatches 22; Indels 25; Gaps 6; OS	Db	34 SNNLCKQCPGMNTHSC-NTTSNTKCDKCPDFTSIPPNSPACSLCRGK--SSNQV 90
Qy	73 BISSCTVDRDTVGCRKNQYRHSENIFQCFNCSLCLNGTVHLSCBQKQNTVC 132	Qy	73 BISSCTVDRDTVGCRKNQYRHSENIFQCFNCSLCLNGTVHLSCBQKQNTVC 132
Db	91 ETKS-CSNTQDPRVC-VASGYCEFEGSN---GCRLCVFQT-----KGSGY 132	Db	91 ETKS-CSNTQDPRVC-VASGYCEFEGSN---GCRLCVFQT-----KGSGY 132
Qy	133 FL--RENBCVSNSCKKELCTKLPOE 160	Qy	133 FL--RENBCVSNSCKKELCTKLPOE 160
Db	133 GVGYSKGDVICKKCPGNDKCDLSFNSID 163	Db	133 GVGYSKGDVICKKCPGNDKCDLSFNSID 163
RESULT 15		RESULT 15	
ID	057091 PRELIMINARY; PRT; 320 AA.	ID	057091 PRELIMINARY; PRT; 320 AA.
AC	057091; SMART; SM00208; TNFR_c6; 2.	AC	057091; SMART; SM00208; TNFR_c6; 2.
DT	01-JUN-1998 (REMBrel. 06, Created)	DT	01-JUN-1998 (REMBrel. 06, Last sequence update)
DT	01-JUN-1998 (REMBrel. 06, Last sequence update)	DT	01-JUN-2002 (REMBrel. 21, Last annotation update)
DR	Tumor necrosis factor receptor II homolog.	DR	Tumor necrosis factor receptor II homolog.
DR	CRMD.	DR	CRMD.
OS	Ectromelia virus.	OS	Ectromelia virus.
OC	Viruses; dsDNA viruses; no RNA stage; Poxviridae; Chordopoxvirinae;	OC	Viruses; dsDNA viruses; no RNA stage; Poxviridae; Chordopoxvirinae;
OX	Orthopoxvirus.	OX	Orthopoxvirus.
NCBI_TaxID=12643;	[1]	NCBI_TaxID=12643;	[1]
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	STRAIN=MUNICH MP3.	RC	STRAIN=MUNICH MP3.
RX	MEDLINE=9818822; PubMed=9520445;	RX	MEDLINE=9818822; PubMed=9520445;
RA	Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,	RA	Loparev V.N., Parsons J.M., Knight J.C., Panus J.F., Ray C.A.,
RA	Buller R.M.L., Pickup D.J., Espiritu J.J.;	RA	Buller R.M.L., Pickup D.J., Espiritu J.J.;
RT	"A third distinct tumor necrosis factor receptor of orthopoxviruses.";	RT	"A third distinct tumor necrosis factor receptor of orthopoxviruses.";
RL	PROC. NATL. ACAD. SCI. U.S.A. 95:3786-3791(1998).	RL	PROC. NATL. ACAD. SCI. U.S.A. 95:3786-3791(1998).
DR	EMBL; U87578; AAC93484; 1; .	DR	EMBL; U87578; AAC93484; 1; .
Qy	126 CTCAGGFL--SENECVCSNCKKSL 150	Qy	126 CTCAGGFL--SENECVCSNCKKSL 150

Page 7

Search completed: December 3, 2002, 14:41:01  
Job time : 33 secs

